

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus.nzp model

Run on: February 4, 2003, 07:18:23 ; Search time 114 Seconds

(without alignments)
303.369 Million cell updates/sec

Title: US-09-817-318-1

Perfect score: 245
Sequence: 1 aattactgtctctctaaag.....taagcacaataaaaaaaa 780

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 129505 seqs, 22169297 residues

Word size: 1

Total number of hits satisfying chosen parameters: 234160

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*

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6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubpaa/PCFUS_PUBCOMB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	11.0	66	US-10-001-843-134	Sequence 134, App
2	7	2.9	115	US-09-925-301-1458	Sequence 1458, App
3	7	2.9	291	US-09-886-055-327	Sequence 327, App
4	7	2.9	355	US-09-789-482-4	Sequence 4, Appl1

5	7	2.9	355	US-09-789-486-4	Sequence 4, Appl1
6	7	2.9	402	US-09-799-777-47	Sequence 47, Appl
7	7	2.9	419	US-10-055-228-5	Sequence 5, Appl1
8	7	2.9	444	US-10-055-228-3	Sequence 3, Appl1
9	7	2.9	449	US-09-910-186A-14	Sequence 14, Appl
10	7	2.9	459	US-09-098-079-22	Sequence 22, Appl
11	7	2.9	595	US-09-925-297-604	Sequence 604, App
12	7	2.9	600	US-09-764-864-1282	Sequence 1282, Ap
13	7	2.9	615	US-09-925-301-1094	Sequence 1094, Ap
14	7	2.9	676	US-09-771-161A-209	Sequence 209, App
15	7	2.9	759	US-09-764-864-823	Sequence 823, App
16	7	2.9	992	US-09-919-408-2	Sequence 2, Appl1
17	7	2.9	992	US-09-872-136-2	Sequence 2, Appl1
18	7	2.9	993	US-09-919-408-4	Sequence 4, Appl1
19	7	2.9	993	US-09-872-136-4	Sequence 4, Appl1
20	7	2.9	1786	US-09-742-096-3	Sequence 3, Appl1
21	7	2.9	2485	US-09-802-669-46	Sequence 46, Appl
22	6	2.4	15	US-09-927-436-10	Sequence 10, Appl
23	6	2.4	16	US-09-805-301-84	Sequence 84, Appl
24	6	2.4	16	US-09-826-752-24	Sequence 24, Appl
25	6	2.4	18	US-09-864-761-38407	Sequence 38407, A
26	6	2.5	20	US-09-984-245-262	Sequence 262, App
27	6	2.4	21	US-09-864-761-37759	Sequence 37759, A
28	6	2.5	25	US-09-864-761-45813	Sequence 45813, A
29	6	2.4	27	US-09-864-761-45698	Sequence 45698, A
30	6	2.5	28	US-08-908-884-6	Sequence 6, Appl1
31	6	2.4	28	US-09-864-761-41603	Sequence 41603, A
32	6	2.5	28	US-09-908-323-6	Sequence 6, Appl1
33	6	2.5	32	US-09-864-761-45704	Sequence 45704, A
34	6	2.5	33	US-08-908-884-8	Sequence 8, Appl1
35	6	2.5	33	US-09-864-761-38783	Sequence 38783, A
36	6	2.5	34	US-09-908-323-8	Sequence 8, Appl1
37	6	2.4	34	US-09-975-143-24	Sequence 24, Appl
38	6	2.5	38	US-09-729-674-26	Sequence 26, Appl
39	6	2.4	40	US-09-865-553-4	Sequence 4, Appl1
40	6	2.4	41	US-09-925-301-1680	Sequence 1680, Ap
41	6	2.5	44	US-09-864-761-42005	Sequence 42005, A
42	6	2.4	45	US-09-764-877-1280	Sequence 1280, Ap
43	6	2.5	46	US-09-873-637-27	Sequence 27, Appl
44	6	2.4	50	US-09-993-844-43	Sequence 43, Appl
45	6	2.4	52	US-09-864-761-45700	Sequence 45700, A

ALIGNMENTS

RESULT 1
US-10-001-843-134
: Sequence 134, Application US/10001843
: Patent No. US20020132255A1
: GENERAL INFORMATION:
: APPLICANT: Salceda, Susana
: APPLICANT: Macina, Roberto
: APPLICANT: Recipon, Herve
: APPLICANT: Caferkey, Herbert
: APPLICANT: Sun, Yongming
: APPLICANT: Liu, Chenghua
: APPLICANT: Turner, Leah
: TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes an
: FILE REFERENCE: DEX-0267
: CURRENT APPLICATION NUMBER: US/10/001,843
: PRIOR FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/249,992
: PRIOR FILING DATE: 2000-11-20
: NUMBER OF SEQ ID NOS: 218
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 134
: LENGTH: 66
: TYPE: PRT
: ORGANISM: Homo sapien
: US-10-001-843-134
Alignment Scores: 1.33e-18 Length: 66
Pred. No.: 66

Score: 27.00 Matches: 27
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.02% Indels: 0
DB: 12 Gaps: 0

US-09-817-318-1 (1-780) x US-10-001-843-134 (1-66)

OY 603 ATGGCGAGGATAAATCAGAGTACTGTCATACAAAGTTATGTTTATGGGTTATTT 662
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Db 1 MeClyArgrgsplyssrsergluvalThrValasnlnysValMetPheTyGlyTyrPhe 20

OY 663 ATAGTCGATAAATTCATTACT 683
|||||
Db 21 lIeGlyAsplysPheIleThr 27

RESULT 2
US-09-925-301-1458
; Sequence 1458, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1458
; LENGTH: 115
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (47)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1458

Alignment Scores:
Pred. No.: 68.7 Length: 115
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-925-301-1458 (1-115)

OY 584 ATCAAAAGATATTAGATAT 604
|||||
Db 40 lIeGlySlyIleuAspAsn 46

RESULT 3
US-09-886-055-327
; Sequence 327, Application US/09886055
; Patent No. US20020132273A1
; GENERAL INFORMATION:
; APPLICANT: STRYER, LUBERT
; APPLICANT: ZOZULYA, SERGEY
; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND
; TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS
; FILE REFERENCE: 078003-0277150
; CURRENT APPLICATION NUMBER: US/09/886,055
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,812
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 522
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 327

; LENGTH: 291
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-886-055-327

Alignment Scores:
Pred. No.: 60.9 Length: 291
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-886-055-327 (1-291)

OY 637 TTATTGACAGTACTGCTGAT 617
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Db 46 LeuIeuThrValThrSerAsp 52

RESULT 4
US-09-789-482-4
; Sequence 4, Application US/09789482
; Patent No. US20020054875A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Alisa E.
; APPLICANT: Ruth, Jeffrey H.
; APPLICANT: Rotman, James B.
; TITLE OF INVENTION: Therapeutic Methods That Target
; TITLE OF INVENTION: Fractalkine or CX3CR1
; FILE REFERENCE: 3238,1000-003
; CURRENT APPLICATION NUMBER: US/09/789,482
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 60/183,568
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355
; TYPE: PRP
; ORGANISM: Homo sapiens
US-09-789-482-4

Alignment Scores:
Pred. No.: 59.3 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-789-482-4 (1-355)

OY 704 TTATTCTCCTGGTTGTAATA 724
|||||
Db 232 LeuIleuValValIle 238

RESULT 5
US-09-789-486-4
; Sequence 4, Application US/09789486
; Patent No. US20020055456A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Alisa E.
; TITLE OF INVENTION: Therapeutic Methods That Target
; TITLE OF INVENTION: Fractalkine or CX3CR1
; FILE REFERENCE: 3238,1000-004
; CURRENT APPLICATION NUMBER: US/09/789,486
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 60/183,568
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 355

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: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-789-486-4

Alignment Scores:
Pred. No.: 59.3 Length: 355
Score: 7.00 Matches: 7
Best Local Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-789-486-4 (1-355)

QY 704 TTATTCCTCGTGTGTAATA 724
Db 232 Leu1leuValVal1le 238

RESULT 6
US-09-799-777-47
: Sequence 47, Application US/09799777
: Patent No. US20020091244A1
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: Hillman, Jennifer L.
: Corley, Neil C.
: Guegler, Karl J.
: Baugh, Mariah
: Sather, Susan
: Shah, Purvi
: TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
: NUMBER OF SEQUENCES: 154
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: INCITE PHARMACEUTICALS, INC.
: STREET: 3174 PORTER DRIVE
: CITY: PALO ALTO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
: CURRENT APPLICATION DATA: US/09/799,777
: APPLICATION NUMBER: US/09/799,777
: FILING DATE: 06-Mar-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/002,485
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: BILLINGS, LUCY J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0459 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650) 855-0555
: TELEFAX: (650) 845-4166
: INFORMATION FOR SEQ ID NO: 47:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 402 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: PANCNOT04
: CLONE: 2084489
: SEQUENCE DESCRIPTION: SEQ ID NO: 47 :
US-09-799-777-47

Alignment Scores:
Pred. No.: 58.3 Length: 402
Score: 7.00 Matches: 7
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-799-777-47 (1-402)

QY 760 GTAAAGCGMAAAAAAAAAA 780
Db 223 VallysAlaLysLysLys 229

RESULT 7
US-10-055-228-5
: Sequence 5, Application US/10055228
: Publication No. US20030022316A1
: GENERAL INFORMATION:
: APPLICANT: Fox, Brian A.
: APPLICANT: Taft, David W.
: APPLICANT: Sheppard, Paul O.
: TITLE OF INVENTION: CUB DOMAIN PROTEIN ZCUB3 AND MATERIALS
: FILE REFERENCE: 00-60
: CURRENT APPLICATION NUMBER: US/10/055,228
: CURRENT FILING DATE: 2002-01-23
: PRIOR APPLICATION NUMBER: 60/263,989
: PRIOR FILING DATE: 2001-01-24
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 5
: LENGTH: 419
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-055-228-5

Alignment Scores:
Pred. No.: 58 Length: 419
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 9 Gaps: 0

US-09-817-318-1 (1-780) x US-10-055-228-5 (1-419)

QY 404 TTGTTAACTAGTTTCTTCG 424
Db 10 Leu1euTherSerPheLeu1eu 16

RESULT 8
US-10-055-228-3
: Sequence 3, Application US/10055228
: Publication No. US20030022316A1
: GENERAL INFORMATION:
: APPLICANT: Fox, Brian A.
: APPLICANT: Taft, David W.
: APPLICANT: Sheppard, Paul O.
: TITLE OF INVENTION: CUB DOMAIN PROTEIN ZCUB3 AND MATERIALS
: FILE REFERENCE: 00-60
: CURRENT APPLICATION NUMBER: US/10/055,228
: CURRENT FILING DATE: 2002-01-23
: PRIOR APPLICATION NUMBER: 60/263,989
: PRIOR FILING DATE: 2001-01-24
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 444
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-055-228-3

Alignment Scores:
Pred. No.: 57.6 Length: 444
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Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 9 Gaps: 0

US-09-817-318-1 (1-780) x US-10-055-228-3 (1-444)

OY 404 TTGTTAACTAGTTTCTCTG 424
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Db 10 LeuLeuThrSerPheLeuLeu 16

RESULT 9

US-09-910-186A-14
; Sequence 14, Application US/09910186A
; Publication No. US2003009025A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research & Material Command
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
; FILE REFERENCE: A33626-A 067252.0107
; CURRENT APPLICATION NUMBER: US/09/910.186A
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/US00/12890
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 09/611,419
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 60/133,865
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/133,866
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/133,867
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/133,868
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/133,869
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 60/133,873
; PRIOR FILING DATE: 1999-05-12
; PRIOR APPLICATION NUMBER: 08/123,975
; PRIOR FILING DATE: 1993-09-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-910-186A-14

Alignment Scores:
Pred. No.: 57.5 Length: 449
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 9 Gaps: 0

US-09-817-318-1 (1-780) x US-09-910-186A-14 (1-449)

OY 607 GCAGGATAATCAGAACTA 627
|||||
Db 164 AlaGlyIleAsnGlnLysLeu 170

RESULT 10

US-09-098-079-22
; Sequence 22, Application US/09098079
; Patent No. US20020064773A1
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Cleveneger, William

APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA

ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Roseman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-09-098-079-22

Alignment Scores:
Pred. No.: 57.3 Length: 459
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-098-079-22 (1-459)

OY 649 AACATACTTGTTATGACA 629
|||||
Db 390 AsnIleThrLeuLeuThr 396

RESULT 11

US-09-925-297-604
; Sequence 604, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (18)


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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (57)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (551)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-297-604

Alignment Scores:
Pred. No.: 55.4      Length: 595
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.92%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-925-297-604 (1-595)

OY 88 TATAGCTACAGCTTTCATCT 68
    |||||||
Db 584 TyrsertyrserPheSerSer 590

RESULT 12
US-09-764-864-1282
; Sequence 1282, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1282
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1282

Alignment Scores:
Pred. No.: 55.4      Length: 600
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.92%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-764-864-1282 (1-600)

OY 303 TTGTAAACGAGACCTTCTT 283
    |||||||
Db 22 PheValasnaGrThrLeuphe 28

RESULT 13
US-09-925-301-1094
; Sequence 1094, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
```

```
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1094
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (113)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (132)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (155)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (157)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1094

Alignment Scores:
Pred. No.: 55.2      Length: 615
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.92%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-925-301-1094 (1-615)

OY 303 TTGTAAACGAGACCTTCTT 283
    |||||||
Db 37 PheValasnaGrThrLeuphe 43

RESULT 14
US-09-771-161A-209
; Sequence 209, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; PRIORITY FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 209
; LENGTH: 676
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-771-161A-209

Alignment Scores:

Pred. No.:	54.5	Length:	676
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	10	Gaps:	0

US-09-817-318-1 (1-780) x US-09-771-161A-209 (1-676)

QY 610 GCGATTAATCAGAGTTACTG 630
|||||

DB 281 GYIYLeasnglnhlsleu 287

RESULT 15

US-09-764-864-823

; Sequence 823, Application US/09764864

; Patent No. US20020132753A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT23

; CURRENT APPLICATION NUMBER: US/09/764,864

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PAM or file wrapper

; NUMBER OF SEQ ID NOS: 1792

; SOFTWARE: Patentln Ver. 2.0

; SEQ ID NO 823

; LENGTH: 759

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (18)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (19)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (21)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (257)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (299)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-764-864-823

Alignment Scores:

Pred. No.:	53.7	Length:	759
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	10	Gaps:	0

US-09-817-318-1 (1-780) x US-09-764-864-823 (1-759)

QY 303 TTTGTAAACAGACCTCTTT 283
|||||

DB 181 PhevalasnaargThrlauphe 187

RESULT 16

US-09-919-408-2

; Sequence 2, Application US/09919408

; Patent No. US20020072077A1

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Thor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL RECEPTORS AND THEIR LIGANDS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/919,408

FILING DATE: 31-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/977,451

FILING DATE: <Unknown>

APPLICATION NUMBER: US 07/906,397

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: US PCT/US92/05401

FILING DATE: 26-JUN-1992

APPLICATION NUMBER: TW 81102961

FILING DATE: 15-APR-1992

APPLICATION NUMBER: US PCT/US92/02750

FILING DATE: 02-APR-1992

APPLICATION NUMBER: US 07/813,593

FILING DATE: 24-DEC-1991

APPLICATION NUMBER: US 07/793,065

FILING DATE: 15-NOV-1991

APPLICATION NUMBER: US 07/728,913

FILING DATE: 28-JUN-1991

APPLICATION NUMBER: US 07/679,666

FILING DATE: 02-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pelt, Irving N.

REGISTRATION NUMBER: 28,601

REFERENCE/DOCKET NUMBER: LEM-3-7P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405

TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 992 amino acids

TYPE: amino acid

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-919-408-2

Alignment Scores:

Pred. No.:	51.9	Length:	992
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	10	Gaps:	0

US-09-817-318-1 (1-780) x US-09-919-408-2 (1-992)

QY 251 CTCTTCAATGACTTGAC 271
|||||

DB 245 Leupherthrlleaspleuasn 251

RESULT 17

US-09-872-136-2

; Sequence 2, Application US/09872136

; Patent No. US20020119545A1

; GENERAL INFORMATION:

; APPLICANT: Lemischka, Thor R.

; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL

```

: RECEPTORS AND THEIR LIGANDS
:
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10014
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/872,136
: FILING DATE: 01-Jun-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/208,786
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US/09/021,324
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US/07/977,451
: FILING DATE: 1992-11-19
: APPLICATION NUMBER: US 07/906,397
: FILING DATE: 26-JUN-1992
: APPLICATION NUMBER: US PCT/US92/05401
: FILING DATE: 26-JUN-1992
: APPLICATION NUMBER: TW 81102961
: FILING DATE: 15-APR-1992
: APPLICATION NUMBER: US PCT/US92/02750
: FILING DATE: 02-APR-1992
: APPLICATION NUMBER: US 07/813,593
: FILING DATE: 24-DEC-1991
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: APPLICATION NUMBER: US 07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Feil, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-7P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 992 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-872-136-2

Alignment Scores:
Pred. No.: 51.9 Length: 992
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-872-136-2 (1-992)
OY 251 CTCCTCACATTGACTTGAC 271
Db 245 Leuphethrllleaspleuash 251

RESULT 18
US-09-919-408-4
```

```

: Sequence 4, Application US/09919408
: Patent No. US20020072077A1
:
: GENERAL INFORMATION:
: APPLICANT: Lemischka, Ihor R.
: TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
: RECEPTORS AND THEIR LIGANDS
:
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10014
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/919,408
: FILING DATE: 31-Jul-2001
: CLASSIFICATION: <Unknown>
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/977,451
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 07/906,397
: FILING DATE: 26-JUN-1992
: APPLICATION NUMBER: US PCT/US92/05401
: FILING DATE: 26-JUN-1992
: APPLICATION NUMBER: TW 81102961
: FILING DATE: 15-APR-1992
: APPLICATION NUMBER: US PCT/US92/02750
: FILING DATE: 02-APR-1992
: APPLICATION NUMBER: US 07/813,593
: FILING DATE: 24-DEC-1991
: APPLICATION NUMBER: US 07/793,065
: FILING DATE: 15-NOV-1991
: APPLICATION NUMBER: US 07/728,913
: FILING DATE: 28-JUN-1991
: APPLICATION NUMBER: US 07/679,666
: FILING DATE: 02-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Feil, Irving N.
: REGISTRATION NUMBER: 28,601
: REFERENCE/DOCKET NUMBER: LEM-3-7P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 993 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-919-408-4

Alignment Scores:
Pred. No.: 51.9 Length: 993
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-919-408-4 (1-993)
OY 251 CTCCTCACATTGACTTGAC 271
Db 244 Leuphethrllleaspleuash 250

RESULT 19
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US-09-872-136-4
; Sequence 4, Application US/09872136
; Patent No. US20020119545A1
; GENERAL INFORMATION:
; APPLICANT: Lemischka, Ihor R.
; TITLE OF INVENTION: TOTIPOTENT HEMATOPOIETIC STEM CELL
; RECEPTORS AND THEIR LIGANDS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varlick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/872,136
; FILING DATE: 01-Jun-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,786
; FILING DATE: <unknown>
; APPLICATION NUMBER: US/09/021,324
; FILING DATE: <unknown>
; APPLICATION NUMBER: US/07/977,451
; FILING DATE: 1992-11-19
; APPLICATION NUMBER: US 07/906,397
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: US PCT/US92/05401
; FILING DATE: 26-JUN-1992
; APPLICATION NUMBER: TW 81102961
; FILING DATE: 15-APR-1992
; APPLICATION NUMBER: US PCT/US92/02750
; FILING DATE: 02-APR-1992
; APPLICATION NUMBER: US 07/813,593
; FILING DATE: 24-DEC-1991
; APPLICATION NUMBER: US 07/793,065
; FILING DATE: 15-NOV-1991
; APPLICATION NUMBER: US 07/728,913
; FILING DATE: 28-JUN-1991
; APPLICATION NUMBER: US 07/679,666
; FILING DATE: 02-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Felt, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: LEM-3-7P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-872-136-4

Alignment Scores:
Pred. No.: 51.9 Length: 993
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
Caps: 0
US-09-817-318-1 (1-780) x US-09-872-136-4 (1-993)

OY 251 CTCCTGACAAATGCATTGAC 271
Db 244 Leuphethrilleaspleunsn 250
RESULT 20
US-09-742-096-3
; Sequence 3, Application US/09742096
; Patent No. US20020155441A1
; GENERAL INFORMATION:
; APPLICANT: DRUILHE, PIERRE
; APPLICANT: DAUBERGES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773USODIV
; CURRENT APPLICATION NUMBER: US/09/742,096
; FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/FR96/00894
; PRIOR FILING DATE: 1996-06-12
; APPLICATION NUMBER: FR 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent In version 3.1
; SEQ ID NO: 3
; LENGTH: 1786
; TYPE: PRT
; ORGANISM: P. falciparum
US-09-742-096-3

Alignment Scores:
Pred. No.: 48 Length: 1786
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
Gaps: 0
US-09-817-318-1 (1-780) x US-09-742-096-3 (1-1786)
OY 760 GTAAGGCCAATAAAAAAAAAA 780
Db 1583 VALLYSALALYSLSYLSLS 1595
RESULT 21
US-09-802-669-46
; Sequence 46, Application US/09802669
; Patent No. US20020004490A1
; GENERAL INFORMATION:
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Marcussen, Eric G.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
; FILE REFERENCE: ISPH-545
; CURRENT APPLICATION NUMBER: US/09/802,669
; FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/665,615
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-669-46

Alignment Scores:
Pred. No.: 46 Length: 2485
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.92% Indels: 0
DB: 10 Gaps: 0
US-09-817-318-1 (1-780) x US-09-802-669-46 (1-2485)
QY 503 CTTTCAAAAGCATGGCTTT 483
|||||
Db 237 LeuserlysserMetGlypne 243
RESULT 22
US-09-927-436-10
; Sequence 10, Application US/09927436
; Patent No. US20020155455A1
; GENERAL INFORMATION:
; APPLICANT: Tadayoni-Rebek, Miltra
; APPLICANT: Amshay, Joseph W.
; APPLICANT: Rooney, Regina
; TITLE OF INVENTION: Highly Homogeneous Molecular Markers for Electrophoresis
; FILE REFERENCE: 0942.5300001
; CURRENT APPLICATION NUMBER: US/09/927,436
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/224,345
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: Modified with TMR
; NAME/KEY: MOD_RES
; LOCATION: (14)..(14)
; OTHER INFORMATION: Modified with TMR
; NAME/KEY: MOD_RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: AMIDATION
US-09-927-436-10
Alignment Scores:
Pred. No.: 870 Length: 15
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45% Indels: 0
DB: 9 Gaps: 0
US-09-817-318-1 (1-780) x US-09-927-436-10 (1-15)
QY 763 AAGGCAAAAAAAAAAAAA 780
|||||
Db 8 LysAlaLysLysLysLys 13
RESULT 23
US-09-805-301-84
; Sequence 84, Application US/09805301
; Patent No. US20020173456A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; APPLICANT: Sparrow, James T.
; APPLICANT: Hauer, Jochen
; APPLICANT: Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700

CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-09-805-301-84
Alignment Scores:
Pred. No.: 863 Length: 16
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45% Indels: 0
DB: 9 Gaps: 0
US-09-817-318-1 (1-780) x US-09-805-301-84 (1-16)
QY 763 AAGGCAAAAAAAAAAAAA 780
|||||
Db 1 LysAlaLysLysLysLys 6
RESULT 24
US-09-826-752-24
; Sequence 24, Application US/09826752
; Patent No. US20010026930A1
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard P.
; APPLICANT: Austriaco Jr., Nicanor
; APPLICANT: Claus, James J.
; APPLICANT: Cole, Francesca
; APPLICANT: Kennedy, Brian
; TITLE OF INVENTION: GENES DETERMINING CELLULAR SENESCENCE IN
; YEAST
; FILE REFERENCE: 0050.1491-005
; CURRENT APPLICATION NUMBER: US/09/826,752
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 08/396,001
; PRIOR FILING DATE: 1995-02-28
; PRIOR APPLICATION NUMBER: PCT/US94/09351
; PRIOR FILING DATE: 1994-08-15
; PRIOR APPLICATION NUMBER: US 08/107,408
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: US 09/323,433
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 48

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-826-752-24

Alignment Scores:
Pred. No.:      863      Length:      16
Score:          6.00      Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.45%      Indels:      0
DB:             10      Gaps:          0

US-09-817-318-1 (1-780) x US-09-826-752-24 (1-16)

OY 236 GCTTACGACCTTACTC 253
DB 10 AAlaEugIntnTrLeu 15

RESULT 25
; Sequence 38407, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
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; SEQ ID NO 38407
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004468.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
US-09-864-761-38407

Alignment Scores:
Pred. No.:      850      Length:      18
Score:          6.00      Matches:      6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    2.45%      Indels:      0
DB:             10      Gaps:          0

US-09-817-318-1 (1-780) x US-09-864-761-38407 (1-18)

OY 388 CCTTATCCAACTCAWTT 405
DB 3 ProleuseAserSerphe 8

RESULT 26
US-09-984-245-262
; Sequence 262, Application US/09984245
; Patent No. US20020165374A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 87 Human Secreted Proteins
; FILE REFERENCE: P2004P1
; CURRENT APPLICATION NUMBER: US/09/984,245
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/154,707
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: PCT/US98/05311
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: US 60/041,277
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/042,344
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,276
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/041,281
; PRIOR FILING DATE: 1997-03-21
; PRIOR APPLICATION NUMBER: US 60/048,094
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,350
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,188
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,135
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/050,937
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,187
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,099
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,352
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,186
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,069
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,095
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; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,131
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,096
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,355
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,160
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,351
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/048,154
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: US 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: US 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 343
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 262
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-262

Alignment Scores:
Pred. No.: 838          Length: 20
Score: 6.00            Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 9                  Gaps: 0

US-09-817-318-1 (1-780) x US-09-984-245-262 (1-20)
OY 742 GAGTCTCCAGAGTCACCA 725
Db 2 GluserProGluserPro 7

RESULT 27
US-09-864-761-37759
; Sequence 37759, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37759
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132642.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.9
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 6.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
US-09-864-761-37759

Alignment Scores:
Pred. No.: 833          Length: 21
Score: 6.00            Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45%      Indels: 0
DB: 10                  Gaps: 0

US-09-817-318-1 (1-780) x US-09-864-761-37759 (1-21)
OY 415 TTTTCTCTGCTGCTCC 432
Db 11 PheServerValseiser 16

RESULT 28
US-09-864-761-45813
; Sequence 45813, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2001-01-30
```



```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,884
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,851
FILING DATE: August 9, 1996
APPLICATION NUMBER: 60/035,166
FILING DATE: January 10, 1997
APPLICATION NUMBER: 60/046,769
FILING DATE: May 16, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-908-884-6

Alignment Scores:
Pred. No.: 802 Length: 28
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50% Indels: 0
DB: 8 Gaps: 0

US-09-817-318-1 (1-780) x US-08-908-884-6 (1-28)

QY 159 TTAGTGAAGTTGCTATT 142
|||||
Db 20 LeuValIysIeuLeu 25

RESULT 31
US-09-864-761-41603
Sequence 41603, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
```

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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 41603
LENGTH: 28
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC008506.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 22
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 16
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 32
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 20
US-09-864-761-41603

Alignment Scores:
Pred. No.: 802 Length: 28
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-864-761-41603 (1-28)

QY 233 ACAGCTTTACAGACCTTA 250
|||||
Db 16 ThrAlaLeuGlnThrIeu 21

RESULT 32
US-09-908-323-6
Sequence 6, Application US/09908323
Patent No. US20020073447A1
GENERAL INFORMATION:
APPLICANT: Dong et al.
TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
```

```
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/908,323
FILING DATE: 17-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/908,884
FILING DATE: <Unknown>
APPLICATION NUMBER: 60/035,166
FILING DATE: January 10, 1997
APPLICATION NUMBER: 60/046,769
FILING DATE: May 16, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/339004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-908-323-6

Alignment Scores:
Pred. No.: 802 Length: 28
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-908-323-6 (1-28)
QY 159 TTGAGCTGCTGCTATTA 142
DB 20 LeuValLysLeuLeuLeu 25

RESULT 33
US-09-864-45704
Sequence 45704, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
```

```
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45704
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC013611.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.52
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.47
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
OTHER INFORMATION: EST_HUMAN HIT: AM812919.1, EVALUDE 7.60e+00
US-09-864-761-45704

Alignment Scores:
Pred. No.: 788 Length: 32
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x US-09-864-761-45704 (1-32)
QY 744 TTGAGCTCCAGAGTCAC 727
DB 4 LeuSerLeuGlnSerHis 9

RESULT 34
US-09-908-884-8
Sequence 8, Application US/08908884
Patent No. US2002013872A1
GENERAL INFORMATION:
APPLICANT: Dong et al.
TITLE OF INVENTION: ACQUIRED RESISTANCE GENES AND USES THEREOF
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
```



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      APPLICATION NUMBER: US/09/908,323
      FILING DATE: 17-Jul-2001
      CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/908,884
      FILING DATE: <Unknown>
      APPLICATION NUMBER: 60/035,166
      FILING DATE: January 10, 1997
      APPLICATION NUMBER: 60/046,769
      FILING DATE: May 16, 1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Elbing, Karen L.
      REGISTRATION NUMBER: 35,238
      REFERENCE/DOCKET NUMBER: 00786/339004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 617-428-0200
      TELEFAX: 617-428-7045
      INFORMATION FOR SEQ ID NO: 8:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 33 amino acids
      TYPE: amino acid
      STRANDEDNESS: single
      TOPOLOGY: linear
      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-908-323-8

Alignment Scores:
Pred. No.: 785
Score: 6.00 Length: 33
Percent Similarity: 100.00% Matches: 6
Best Local Similarity: 100.00% Conservative: 0
Query Match: 2.50% Mismatches: 0
DB: 10 Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x US-09-908-323-8 (1-33)
QY 159 TTAGTGAGTGGCTATTGA 142
Db 17 LeuValLysLeuLeuLeu 22

RESULT 37
US-09-975-143-24
; Sequence 24, Application US/09975143
; Patent No. US20020155513A1
; GENERAL INFORMATION:
; APPLICANT: HSU, Daniel, K.
; APPLICANT: LIU, Fu-tong
; TITLE OF INVENTION: GALECTIN EXPRESSION IS INDUCED IN
; FILE REFERENCE: CIRRHOTIC LIVER AND HEPATOCELLULAR CARCINOMA
; CURRENT APPLICATION NUMBER: US/09/975,143
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: PCT/US00/08561
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: nematode
US-09-975-143-24

Alignment Scores:
Pred. No.: 782
Score: 6.00 Length: 34
Percent Similarity: 100.00% Matches: 6
Best Local Similarity: 100.00% Conservative: 0
Query Match: 2.45% Mismatches: 0
DB: 9 Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x US-09-975-143-24 (1-34)

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      QY 379 CATCGCTTTCCTTATCC 396
      Db 7 HisArgLeuProLeuSer 12

RESULT 38
US-09-729-674-26
; Sequence 26, Application US/09729674
; Patent No. US20010039335A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Werberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Agostino, Michael J.
; APPLICANT: Steindinger II, Robert J.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; TITLE OF INVENTION: GENETICS INSTITUTE, INC.
; FILE REFERENCE: 6055-64X
; CURRENT APPLICATION NUMBER: US/09/729,674
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 09/539,330
; NUMBER OF SEQ ID NOS: 283
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-674-26

Alignment Scores:
Pred. No.: 771
Score: 6.00 Length: 38
Percent Similarity: 100.00% Matches: 6
Best Local Similarity: 100.00% Conservative: 0
Query Match: 2.50% Mismatches: 0
DB: 10 Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x US-09-729-674-26 (1-38)
QY 774 TTTTGTGCTTACACC 757
Db 12 PhePheCysLeuTyrThr 17

RESULT 39
US-09-865-553-4
; Sequence 4, Application US/09865553
; Patent No. US20020055174A1
; GENERAL INFORMATION:
; APPLICANT: Riltner, Karola
; APPLICANT: Jacobs, Eric
; TITLE OF INVENTION: Complex for Transferring an Anionic Substance of Interest
; FILE REFERENCE: 032751-050
; CURRENT APPLICATION NUMBER: US/09/865,553
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/246,083
; PRIOR FILING DATE: 2000-11-07
; PRIOR APPLICATION NUMBER: US 60/277,982
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00440162.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: EP 01440049.3
; PRIOR FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1

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: SEQ ID NO 4
: LENGTH: 40
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: JTS-1-K13
US-09-865-553-4

Alignment Scores:
Pred. No.: 766      Length: 40
Score: 6.00        Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.45%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-865-553-4 (1-40)
QY 763 AAGCGAAGGCTCTGT 296
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Db 24 LysAlaLysLysLysLys 29

RESULT 40
US-09-925-301-1680
: Sequence 1680, Application US/09925301
: Patent No. US20020052308A1
: GENERAL INFORMATION:
: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
: FILE REFERENCE: PA106
: CURRENT FILING DATE: 2001-08-10
: PRIOR APPLICATION NUMBER: PCT/US00/05882
: PRIOR FILING DATE: 2000-03-08
: PRIOR APPLICATION NUMBER: 60/124,270
: PRIOR FILING DATE: 1999-03-12
: NUMBER OF SEQ ID NOS: 1694
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1680
: LENGTH: 41
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-925-301-1680

Alignment Scores:
Pred. No.: 763      Length: 41
Score: 6.00        Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.45%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-925-301-1680 (1-41)
QY 279 TCACAAAGGCTCTGT 296
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Db 5 SerGlnAtgGlySerCys 10

RESULT 41
US-09-864-761-42005
: Sequence 42005, Application US/09864761
: Patent No. US20020048763A1
: GENERAL INFORMATION:
: APPLICANT: Penn, Sharon G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, David K.
: APPLICANT: Chen, Wensheng
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
: TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
: FILE REFERENCE: Aecmica-X-1
: CURRENT APPLICATION NUMBER: US/09/864,761
: CURRENT FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/180,312
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: PRIOR FILING DATE: 2000-02-04
: PRIOR APPLICATION NUMBER: US 60/207,456
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: US 09/632,366
: PRIOR FILING DATE: 2000-08-03
: PRIOR APPLICATION NUMBER: JTS 24263, 6
: PRIOR FILING DATE: 2000-10-04
: PRIOR APPLICATION NUMBER: US 60/236,359
: PRIOR FILING DATE: 2000-09-27
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00669
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00662
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00661
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 60/234,687
: PRIOR FILING DATE: 2000-09-21
: PRIOR APPLICATION NUMBER: US 09/608,408
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: US 09/774,203
: PRIOR FILING DATE: 2001-01-29
: NUMBER OF SEQ ID NOS: 49117
: SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
: SEQ ID NO 42005
: LENGTH: 44
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO AC011989.3
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.9
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.2
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.5
: OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.9
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.1
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
: OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.7
: OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
: OTHER INFORMATION: EST_HUMAN HIT: AW52219.1, EVALUATE 2.00e-19
: OTHER INFORMATION: SWISSPROT HIT: P02775, EVALUATE 1.00e-20
US-09-864-761-42005

Alignment Scores:
Pred. No.: 756      Length: 44
Score: 6.00        Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.50%      Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-864-761-42005 (1-44)
QY 441 ATAGCAAGGACTCAC 424
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Db 33 IleGlyLysGlyThrHis 38

RESULT 42
US-09-764-877-1280
: Sequence 1280, Application US/09764877
: Patent No. US20020147140A1
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1280
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1280

Alignment Scores:
Pred. No.: 754      Length: 45
Score: 6.00         Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45%  Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-764-877-1280 (1-45)
QY 418 TCTTCTGTGAGTTCCTTT 435
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DB 38 SerSerValSerSerPhe 43

RESULT 43
US-09-873-637-27
; Sequence 27, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 27
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-27

Alignment Scores:
Pred. No.: 752      Length: 46
Score: 6.00         Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.50%  Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-873-637-27 (1-46)
QY 447 TCAATATAGGCAAGGA 430
      |||||||
DB 10 SerIleIleIlylVysIly 15

RESULT 44
US-09-993-844-43
; Sequence 43, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
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; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-993-844-43

Alignment Scores:
Pred. No.: 744      Length: 50
Score: 6.00         Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.45%  Indels: 0
DB: 10              Gaps: 0

US-09-817-318-1 (1-780) x US-09-993-844-43 (1-50)
QY 415 TTTTCTGTGAGTTC 432
      |||||||
DB 8 PheSerSerValSerSer 13

RESULT 45
US-09-864-761-45700
; Sequence 45700, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45700
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC021385.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
; OTHER INFORMATION: EST_HUMAN HIT: A1932673.1, EVALUE 6.50e+00
US-09-864-761-45700

Alignment Scores:
Pred. No.: 740          Length: 52
Score: 6.00           Matches: 6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 2.45%              Indels: 0
DB: 10                        Gaps: 0

US-09-817-318-1 (1-780) x US-09-864-761-45700 (1-52)
OY 415 TTTTCTCTGTGAGTTC 432
Db 44 PheserValSerSer 49
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Search completed: February 4, 2003, 07:28:17
Job time : 123 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 4, 2003, 07:17:33 : Search time 23.5 Seconds
(without alignments)
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Title: US-09-817-318-1

Perfect score: 245
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 262574 seqs, 29422922 residues

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Total number of hits satisfying chosen parameters: 438908

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Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2.9	7	21	1	US-08-231-730A-31
2	2.9	7	21	1	US-08-427-001C-31
3	2.9	7	21	1	US-08-457-798-31
4	2.9	7	21	1	US-08-457-171-31
5	2.9	7	21	1	US-08-505-486-31
6	2.9	7	21	2	US-08-689-489C-31
7	2.9	7	21	3	US-08-801-028-31
8	2.9	7	21	3	US-09-340-154-31
9	2.9	7	21	4	US-09-222-802A-31
10	2.9	7	21	4	US-09-462-611B-31
11	2.9	7	21	5	PCT-US94-06176-31
12	2.9	7	21	5	PCT-US94-12550-31

13	7	2.9	21	5	PCT-US95-04335-31	Sequence 31, Appl
14	7	2.9	21	5	PCT-US95-04718-31	Sequence 31, Appl
15	7	2.9	21	5	PCT-US95-09338-31	Sequence 31, Appl
16	7	2.9	21	5	PCT-US95-09339-31	Sequence 31, Appl
17	7	2.9	38	2	US-08-484-905-85	Sequence 85, Appl
18	7	2.9	38	3	US-08-481-985B-85	Sequence 85, Appl
19	7	2.9	38	4	US-08-370-476-85	Sequence 85, Appl
20	7	2.9	42	2	US-08-484-905-86	Sequence 86, Appl
21	7	2.9	42	3	US-08-481-985B-86	Sequence 86, Appl
22	7	2.9	42	4	US-08-370-476-86	Sequence 86, Appl
23	7	2.9	97	4	US-09-366-887A-6	Sequence 6, Appl
24	7	2.9	98	4	US-09-366-887A-7	Sequence 7, Appl
25	7	2.9	105	4	US-09-071-035-292	Sequence 292, Appl
26	7	2.9	107	4	US-09-069-023-14	Sequence 14, Appl
27	7	2.9	131	4	US-09-071-035-290	Sequence 290, Appl
28	7	2.9	206	4	US-09-134-001C-5047	Sequence 5047, Appl
29	7	2.9	207	4	US-09-415-522-2	Sequence 2, Appl
30	7	2.9	219	4	US-09-069-023-12	Sequence 12, Appl
31	7	2.9	226	4	US-09-134-001C-5494	Sequence 5494, Appl
32	7	2.9	350	2	US-08-484-905-65	Sequence 65, Appl
33	7	2.9	350	2	US-08-484-905-67	Sequence 67, Appl
34	7	2.9	350	3	US-08-481-985B-65	Sequence 65, Appl
35	7	2.9	350	3	US-08-481-985B-67	Sequence 67, Appl
36	7	2.9	350	4	US-08-370-476-65	Sequence 65, Appl
37	7	2.9	350	4	US-08-370-476-67	Sequence 67, Appl
38	7	2.9	355	1	US-08-153-848-28	Sequence 28, Appl
39	7	2.9	355	1	US-08-153-848-32	Sequence 32, Appl
40	7	2.9	355	3	US-09-299-843A-28	Sequence 28, Appl
41	7	2.9	355	3	US-09-299-843A-32	Sequence 32, Appl
42	7	2.9	355	4	US-09-088-337B-28	Sequence 28, Appl
43	7	2.9	355	4	US-09-088-337B-32	Sequence 32, Appl
44	7	2.9	355	5	PCT-US93-11153-28	Sequence 28, Appl
45	7	2.9	355	5	PCT-US93-11153-32	Sequence 32, Appl

ALIGNMENTS

RESULT 1
US-08-231-730A-31
Sequence 31, Application US/08231730A
Patent No. 5561107
GENERAL INFORMATION:
APPLICANT: JAYNES, JESSE M.
TITLE OF INVENTION: METHOD OF ENHANCING WOUND HEALING BY STIMULATING FIBROBLASTS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEVEN J. HOUTLOUIS
ADDRESS: INTELLECTUAL PROPERTY/TECHNOLOGY LAW
STREET: 200 PARK DRIVE, SUITE 210
CITY: P.O. BOX 14329
STATE: RESEARCH TRIANGLE PARK
COUNTRY: NORTH CAROLINA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
OPERATING SYSTEM: MACINTOSH
SOFTWARE: M.S. WORD 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,730A
FILING DATE: 04-20-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,476
FILING DATE: 04-08-94
APPLICATION NUMBER: 08/039,620
FILING DATE: 06-04-93
APPLICATION NUMBER: 08/148,491
FILING DATE: 11-08-93
APPLICATION NUMBER: 08/148,889
FILING DATE: 11-08-93
ATTORNEY/AGENT INFORMATION:

NAME: HULTQUIST, STEVEN J.
REGISTRATION NUMBER: 28021
REFERENCE/DOCKET NUMBER: 4013-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)990-9531
TELEFAX: (919)990-9532
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 21
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: NO
FRAGMENT TYPE: COMPLETE PEPTIDE
ORIGINAL SOURCE: SYNTHETIC
IMMEDIATE SOURCE: SYNTHETIC
PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
US-08-231-730A-31

Alignment Scores:
Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-231-730A-31 (1-21)

OY 760 GTAAAGCAAAAAAAAAAAAAA 780

Db 15 VallysAlaLysLysLysLys 21

RESULT 2

US-08-427-001C-31

Sequence 31, Application US/08427001C

Patent No. 5717064

GENERAL INFORMATION:

APPLICANT: JULIAN, GORDON R.

TITLE OF INVENTION: METHYLATED LYSINE-RICH LYTIIC PEPTIDES.

TITLE OF INVENTION: AND METHOD OF MAKING THE SAME BY REDUCTIVE ALKYLATION

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

STREET: 555 Thirteenth Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE

COMPUTER: IBM COMPATIBLE

OPERATING SYSTEM: DOS

SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/427,001C

FILING DATE: 24-APR-95

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/148,889

FILING DATE: 08-NOV-93

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: WALKER, BARBARA W.

REGISTRATION NUMBER: 35,400

REFERENCE/DOCKET NUMBER: 2093-105A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)783-6040

TELEFAX: (202)783-6031

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-427-001C-31

Alignment Scores:
Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-427-001C-31 (1-21)

OY 760 GTAAAGCAAAAAAAAAAAAAA 780

Db 15 VallysAlaLysLysLysLys 21

RESULT 3

US-08-457-798-31

Sequence 31, Application US/08457798

Patent No. 5744445

GENERAL INFORMATION:

APPLICANT: JAYNES, JESSE M.

APPLICANT: JULIAN, GORDON R.

TITLE OF INVENTION: METHOD OF TREATING PULMONARY DISEASE

TITLE OF INVENTION: STATES WITH NON-NATURALLY OCCURRING

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: JESSE M. JAYNES,

ADDRESS: DEMETER BIOTECHNOLOGIES, LTD.

STREET: 150 FAYETTEVILLE ST. MALL, SUITE 2700

CITY: RALEIGH

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27601

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE

COMPUTER: APPLE MACINTOSH

OPERATING SYSTEM: MACINTOSH

SOFTWARE: M.S. WORD 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/457,798

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/039,620A

FILING DATE: 19930604

ATTORNEY/AGENT INFORMATION:

NAME: HULTQUIST, STEVEN J.

REGISTRATION NUMBER: 28021

REFERENCE/DOCKET NUMBER: 4013-103

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)990-9531

TELEFAX: (919)990-9532

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE:

DESCRIPTION: PEPTIDE

HYPOTHETICAL: NO

FRAGMENT TYPE: COMPLETE PEPTIDE

ORIGINAL SOURCE: SYNTHETIC

IMMEDIATE SOURCE: SYNTHETIC

PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED

US-08-457-798-31

Alignment Scores:

Pred. No.: 107

Length: 21

Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-457-798-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAA 780

DB 15 VallysAlatylsLysLysLys 21

RESULT 4

US-08-457-171-31
; Sequence 31, Application US/08457171
; Patent No. 5773413
; GENERAL INFORMATION:
; APPLICANT: JAYNES, JESSE M.
; APPLICANT: JULIAN, GORDON R.
; TITLE OF INVENTION: METHOD OF COMBATTING MAMMALIAN NEOPLASIA, AND LYTIC PEPTIDES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STEVEN J. HULTQUIST
; ADDRESSEE: INTELLECTUAL PROPERTY/TECHNOLOGY LAW
; STREET: 200 PARK DRIVE, SUITE 210
; STREET: P.O. BOX 14329
; CITY: RESEARCH TRIANGLE PARK
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
; OPERATING SYSTEM: MACINTOSH
; SOFTWARE: M.S. WORD 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,171
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,476A
; FILING DATE: 04-08-94
; APPLICATION NUMBER: 08/039,620
; FILING DATE: 06-04-93
; APPLICATION NUMBER: 08/148,491
; FILING DATE: 11-08-93
; APPLICATION NUMBER: 08/148,889
; FILING DATE: 11-08-93
; ATTORNEY/AGENT INFORMATION:
; NAME: HULTQUIST, STEVEN J.
; REGISTRATION NUMBER: 28021
; REFERENCE/DOCKET NUMBER: 4013-106
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)990-9531
; TELEFAX: (919)990-9532
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: NO
; HYPOTHETICAL: NO
; FRAGMENT TYPE: COMPLETE PEPTIDE
; ORIGINAL SOURCE: SYNTHETIC
; IMMEDIATE SOURCE: SYNTHETIC
; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
US-08-457-171-31

Alignment Scores:

Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-457-171-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAA 780

DB 15 VallysAlatylsLysLysLys 21

RESULT 5

US-08-505-486-31
; Sequence 31, Application US/08505486
; Patent No. 5955573
; GENERAL INFORMATION:
; APPLICANT: Jesse M. Jaynes
; TITLE OF INVENTION: UBIQUITIN-LYTIC PEPTIDE FUSION GENE
; CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND
; TITLE OF INVENTION: METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 Thirteenth Street N.W.
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,486
; FILING DATE: 21-JUL-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/279,472
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, BARBARA W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 2093-117A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: NO
; HYPOTHETICAL: NO
; FRAGMENT TYPE: COMPLETE PEPTIDE
; ORIGINAL SOURCE: SYNTHETIC
; IMMEDIATE SOURCE: SYNTHETIC
; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
US-08-505-486-31

Alignment Scores:

Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x US-08-505-486-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAA 780

DB 15 VallysAlatylsLysLysLys 21

RESULT 6
US-08-689-489C-31
; Sequence 31, Application US/08689489C
; Patent No. 6001805
; GENERAL INFORMATION:
; APPLICANT: Jesse M. Jaynes, Gordon R. Julian
; TITLE OF INVENTION: Method of Enhancing Wound Healing By
; TITLE OF INVENTION: Stimulating Fibro-blast and Keratinocyte Growth In
; TITLE OF INVENTION: Vivo, Utilizing Amphipathic Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohnwell, Flg9, Ernst & Kurz
; STREET: 555 13TH STREET
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,489C
; FILING DATE: August 12, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/231,730
; FILING DATE: April 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,476
; FILING DATE: April 8, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,620
; FILING DATE: June 4, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/148,889
; FILING DATE: No. 6001805ember 8, 1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/148,491
; FILING DATE: No. 6001805ember, 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark I. Bowditch
; REGISTRATION NUMBER: 40,315
; REFERENCE/DOCKET NUMBER: 2093-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: linear
; US-08-689-489C-31

Alignment Scores:
Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-689-489C-31 (1-21)
QY 760 GTAAAGCAAAAAAAAAAAAAA 780
DB 15 VallysAlatylsLysLys 21

RESULT 7
US-08-801-028-31
; Sequence 31, Application US/08801028
; Patent No. 6018102
; GENERAL INFORMATION:
; APPLICANT: JOAN GARBARINO
; APPLICANT: JESSE M. JAYNES
; APPLICANT: WILLIAM BELKNAP
; TITLE OF INVENTION: UBIQUITIN-LYTIC PEPTIDE FUSION GENE CONSTRUCTS, PROTEIN PRO
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STEVEN J. HULTQUIST
; ADDRESSEE: INTELLECTUAL PROPERTY/TECHNOLOGY LAW
; STREET: 200 PARK DRIVE, SUITE 210
; STREET: P.O. BOX 14329
; CITY: RESEARCH TRIANGLE PARK
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
; COMPUTER: APPLE MACINTOSH
; OPERATING SYSTEM: MACINTOSH
; SOFTWARE: M.S. WORD 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,028
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,472
; FILING DATE: JULY 22, 1994
; APPLICATION NUMBER: 08/225,476
; FILING DATE: 04-20-94
; APPLICATION NUMBER: 08/225,476
; FILING DATE: 04-08-94
; APPLICATION NUMBER: 08/039,620
; FILING DATE: 06-04-93
; APPLICATION NUMBER: 08/148,491
; FILING DATE: 11-08-93
; APPLICATION NUMBER: 08/148,889
; FILING DATE: 11-08-93
; ATTORNEY/AGENT INFORMATION:
; NAME: WASSERMAN, FRAN S.
; REGISTRATION NUMBER: 34,273
; REFERENCE/DOCKET NUMBER: 4013-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)990-9531
; TELEFAX: (919)990-9532
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: NO
; HYPOTHETICAL: NO
; FRAGMENT TYPE: COMPLETE PEPTIDE
; ORIGINAL SOURCE: SYNTHETIC
; IMMEDIATE SOURCE: SYNTHETIC
; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
; US-08-801-028-31

Alignment Scores:
Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-801-028-31 (1-21)
QY 760 GTAAAGCAAAAAAAAAAAAAA 780
DB 15 VallysAlatylsLysLys 21

Db 15 VallysAlaLysLysLysLys 21

RESULT 8

US-09-340-154-31

; Sequence 31, Application US/09340154

; Patent No. 6084156

; GENERAL INFORMATION:

; APPLICANT: Jesse M. Jaynes

; TITLE OF INVENTION: UBIQUITIN-LYTIC PEPTIDE FUSION GENE

; TITLE OF INVENTION: CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND

; TITLE OF INVENTION: METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ

; STREET: 555 Thirteenth Street N.W.

; CITY: Washington

; STATE: D. C.

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE

; COMPUTER: IBM COMPATIBLE

; OPERATING SYSTEM: DOS

; SOFTWARE: WordPerfect 5.1+

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/340,154

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/505,486

; FILING DATE: 21-JUL-1995

; APPLICATION NUMBER: U.S. 08/279,472

; FILING DATE: 22-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WALKER, BARBARA W.

; REGISTRATION NUMBER: 35,400

; REFERENCE/DOCKET NUMBER: 2093-117A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)783-6040

; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21

; TYPE: AMINO ACID

; TOPOLOGY: LINEAR

; MOLECULE TYPE:

; DESCRIPTION: PEPTIDE

; HYPOTHEICAL: NO

; FRAGMENT TYPE: COMPLETE PEPTIDE

; ORIGINAL SOURCE: SYNTHETIC

; IMMEDIATE SOURCE: SYNTHETIC

; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED

US-09-340-154-31

Alignment Scores:

Pred. No.:	107	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	3	Gaps:	0

US-09-817-318-1 (1-780) x US-09-340-154-31 (1-21)

QY 760 GTAAGGCAAAAAAAAAAAAA 780

|||||

Db 15 VallysAlaLysLysLysLys 21

RESULT 9

US-09-232-802A-31

; Sequence 31, Application US/09232802A

; Patent No. 6191110

; GENERAL INFORMATION:

; APPLICANT: Jesse M. Jaynes, Gordon R. Julian

; TITLE OF INVENTION: Method of Enhancing Wound Healing By

; Stimulating Fibro-blast and Keratinocyte Growth In

; Vivo, Utilizing Amphipathic Peptides

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Manbeck

; STREET: 555 13TH STREET

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/232,802A

; FILING DATE: 19-Jan-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/689,489

; FILING DATE: August 12, 1996

; APPLICATION NUMBER: US 08/231,730

; FILING DATE: April 20, 1994

; APPLICATION NUMBER: US 08/225,476

; FILING DATE: April 8, 1994

; APPLICATION NUMBER: US 08/039,620

; FILING DATE: June 4, 1993

; APPLICATION NUMBER: 08/148,889

; FILING DATE: No. 6191110ember 8, 1993

; APPLICATION NUMBER: 08/148,491

; FILING DATE: No. 6191110ember, 8, 1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark I. Bowditch

; REGISTRATION NUMBER: 40,315

; REFERENCE/DOCKET NUMBER: 2093-142

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-783-6040

; TELEFAX: 202-783-6031

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 21 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHEICAL: NO

; FRAGMENT TYPE: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-09-232-802A-31

Alignment Scores:

Pred. No.:	107	Length:	21
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x US-09-232-802A-31 (1-21)

QY 760 GTAAGGCAAAAAAAAAAAAA 780

|||||

Db 15 VallysAlaLysLysLysLys 21

RESULT 10

US-09-482-611B-31

; Sequence 31, Application US/09482611B

; Patent No. 6448391

; GENERAL INFORMATION:

; APPLICANT: Garbarino, Joan

; APPLICANT: Belknap, William

;; TITLE OF INVENTION: Ubiquitin-Lytic Peptide Fusion Gene Constructs, Protein Products
;; FILE REFERENCE: 2093-149
;; CURRENT APPLICATION NUMBER: US/09/482,611B
;; PRIOR FILING DATE: 2000-01-14
;; PRIOR APPLICATION NUMBER: US 08/801,028
;; PRIOR FILING DATE: 1997-02-19
;; PRIOR APPLICATION NUMBER: US 08/279,472
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 31
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Lytic Peptide
US-09-482-611B-31

Alignment Scores:
Pred. No.: 107
Score: 7.00 Length: 21
Percent Similarity: 100.00% Matches: 7
Best Local Similarity: 100.00% Conservative: 0
Query Match: 2.86% Mismatches: 0
DB: Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x US-09-482-611B-31 (1-21)

QY 760 GTAAGCGCAAAAAAAAAAAAAA 780
Db 15 VallysAlalyslsylslys 21

RESULT 11
PCT-US94-06176-31

;; Sequence 31, Application PC/TUS9406176
;; GENERAL INFORMATION:
;; APPLICANT: DEMETER BIOTECHNOLOGIES
;; TITLE OF INVENTION: METHOD OF TREATING PULMONARY DISEASE STATES WITH NON-NATURALLY
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FRAN S. WASSERMAN
;; ADDRESS: INTELLECTUAL PROPERTY/
;; STREET: 200 PARK DRIVE, SUITES 209 & 210
;; CITY: RESEARCH TRIANGLE PARK
;; STATE: NORTH CAROLINA
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;; COMPUTER: APPLE MACINTOSH
;; OPERATING SYSTEM: MACINTOSH
;; SOFTWARE: M.S. WORD 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/06176
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: U.S.08/0039,620
;; FILING DATE: 04-06-93
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: WASSERMAN, FRAN S.
;; REGISTRATION NUMBER: 34,273
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)990-9531
;; TELEFAX: (919)990-9532
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21
;; TYPE: AMINO ACID

;; TOPOLOGY: LINEAR
;; MOLECULE TYPE:
;; DESCRIPTION: PEPTIDE
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: COMPLETE PEPTIDE
;; ORIGINAL SOURCE: SYNTHETIC
;; IMMEDIATE SOURCE: SYNTHETIC
;; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
PCT-US94-06176-31

Alignment Scores:
Pred. No.: 107
Score: 7.00 Length: 21
Percent Similarity: 100.00% Matches: 7
Best Local Similarity: 100.00% Conservative: 0
Query Match: 2.86% Mismatches: 0
DB: Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x PCT-US94-06176-31 (1-21)

QY 760 GTAAGCGCAAAAAAAAAAAAAA 780
Db 15 VallysAlalyslsylslys 21

RESULT 12
PCT-US94-12550-31

;; Sequence 31, Application PC/TUS9412550
;; GENERAL INFORMATION:
;; APPLICANT: JULIAN, GORDON R.
;; TITLE OF INVENTION: METHYLATED LYSINE-RICH LYTC
;; TITLE OF INVENTION: PEPTIDES AND METHOD OF
;; TITLE OF INVENTION: MAKING SAME BY REDUCTIVE
;; NUMBER OF SEQUENCES: 37
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STEVEN J. HULTQUIST
;; ADDRESS: INTELLECTUAL PROPERTY/TECHNOLOGY LAW
;; STREET: 200 PARK DRIVE, SUITE 210
;; CITY: RESEARCH TRIANGLE PARK
;; STATE: NORTH CAROLINA
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE
;; COMPUTER: APPLE MACINTOSH
;; OPERATING SYSTEM: MACINTOSH
;; SOFTWARE: M.S. WORD 5.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/12550
;; FILING DATE: NOVEMBER 8, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: HULTQUIST, STEVEN J.
;; REGISTRATION NUMBER: 28021
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919)990-9531
;; TELEFAX: (919)990-9532
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21
;; TYPE: AMINO ACID
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE:
;; DESCRIPTION: PEPTIDE
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: COMPLETE PEPTIDE
;; ORIGINAL SOURCE: SYNTHETIC
;; IMMEDIATE SOURCE: SYNTHETIC
;; PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED
PCT-US94-12550-31

Alignment Scores:

Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x PCT-US95-04335-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAAAAAA 780

Db 15 VallysAlatylslyslslys 21

RESULT 13

PCT-US95-04335-31
Sequence 31, Application PC/TUS9504335

GENERAL INFORMATION:

APPLICANT: JAYNES, JESSE M.

APPLICANT: JULIAN, GORDON R.

TITLE OF INVENTION: METHOD OF COMBATING MAMMALIAN NEOPLASIA, AND LYTIC PEPTIDES

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FRAN S. WASSERMAN

ADDRESSEE: INTELLECTUAL PROPERTY/TECHNOLOGY LAW

STREET: 200 PARK DRIVE, SUITE 210

STREET: P.O. BOX 14329

CITY: RESEARCH TRIANGLE PARK

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE

COMPUTER: APPLE MACINTOSH

OPERATING SYSTEM: MACINTOSH

SOFTWARE: M.S. WORD 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04335

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USA08/225,476

FILING DATE: 04-08-94

ATTORNEY/AGENT INFORMATION:

NAME: WASSERMAN, FRAN S.

REGISTRATION NUMBER: 34273

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)990-9531

TELEFAX: (919)990-9532

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE:

DESCRIPTION: PEPTIDE

HYPOTHETICAL: NO

FRAGMENT TYPE: COMPLETE PEPTIDE

ORIGINAL SOURCE: SYNTHETIC

IMMEDIATE SOURCE: SYNTHETIC

PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED

PCT-US95-04335-31

Alignment Scores:

Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x PCT-US95-04335-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAAAAAA 780

Db 15 VallysAlatylslyslslys 21

RESULT 14

PCT-US95-04718-31
Sequence 31, Application PC/TUS9504718

GENERAL INFORMATION:

APPLICANT: DEMETER BIOTECHNOLOGIES, LTD.

TITLE OF INVENTION: METHOD OF ENHANCING WOUND HEALING BY STIMULATING FIBROBLAST

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESSES:

ADDRESSEE: FRAN S. WASSERMAN

ADDRESSEE: INTELLECTUAL PROPERTY/TECHNOLOGY LAW

STREET: 200 PARK DRIVE, SUITE 210

STREET: P.O. BOX 14329

CITY: RESEARCH TRIANGLE PARK

STATE: NORTH CAROLINA

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.4 MB STORAGE

COMPUTER: APPLE MACINTOSH

OPERATING SYSTEM: MACINTOSH

SOFTWARE: M.S. WORD 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04718

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/231,730

FILING DATE: 20-04-94

ATTORNEY/AGENT INFORMATION:

NAME: WASSERMAN, FRAN S.

REGISTRATION NUMBER: 34273

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)990-9531

TELEFAX: (919)990-9532

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 21

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE:

DESCRIPTION: PEPTIDE

HYPOTHETICAL: NO

FRAGMENT TYPE: COMPLETE PEPTIDE

ORIGINAL SOURCE: SYNTHETIC

IMMEDIATE SOURCE: SYNTHETIC

PUBLICATION INFORMATION: NOT PREVIOUSLY PUBLISHED

PCT-US95-04718-31

Alignment Scores:

Pred. No.: 107 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x PCT-US95-04718-31 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAAAAAA 780

Db 15 VallysAlatylslyslslys 21

RESULT 15

PCT-US95-09338-31

Sequence 31, Application PC/TUS9509338

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: UBIQUITIN-LYTIC PEPTIDE FUSION GENE

CONSTRUCTS, PROTEIN PRODUCTS DERIVING THEREFROM, AND

IMMEDIATE SOURCE: SYNTHETIC

US-08-484-905-85

Alignment Scores:

Alignment Scores:
Pred. No.: 99 Length: 38
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x US-08-484-905-85 (1-38)

OY 625 ACTTGATTTATCCCTGCC 605

Db 19 ThrsrAspLeuSerLeuPro 25

RESULT 18

US-08-481-985B-85
; Sequence 85, Application US/08481985B
; Patent No. 6011146
; GENERAL INFORMATION:
; APPLICANT: Motiez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,985B
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0106-04000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14..15
; OTHER INFORMATION: /note="Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
US-08-481-985B-85

Alignment Scores:

Alignment Scores:
Pred. No.: 99 Length: 38
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Mismatches: 0
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-481-985B-85 (1-38)

OY 625 ACTTGATTTATCCCTGCC 605

Db 19 ThrsrAspLeuSerLeuPro 25

RESULT 19

US-08-370-476-85
; Sequence 85, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Motiez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castrouge, Amanda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESS: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370,476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 14..15
; OTHER INFORMATION: /note="Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
US-08-370-476-85

Alignment Scores:

Alignment Scores:
Pred. No.: 99 Length: 38
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Mismatches: 0
Conservative: 0

Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 4 Gaps: 0

US-09-817-318-1 (1-780) x US-08-370-476-85 (1-38)

OY 625 ACTTGTGATTATCCCTGCC 605
|||||
Db 19 ThrsrAspLeuSerLeuPro 25

RESULT 20

US-08-484-905-86

; Sequence 86, Application US/08484905

; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunnet

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/484,905

; FILING DATE: 07-JUNE-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Potler, Jane E. R.

; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 03495.0106-03000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 86:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 18..19

; OTHER INFORMATION:

; OTHER INFORMATION: /note= "Xaa is an unidentified

; amino acid residue."

; US-08-484-905-86

Alignment Scores:

Pred. No.: 97.7 Length: 42

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x US-08-484-905-86 (1-42)

OY 625 ACTTGTGATTATCCCTGCC 605
|||||
Db 23 ThrsrAspLeuSerLeuPro 29

RESULT 21

US-08-481-985B-86

; Sequence 86, Application US/08481985B

; Patent No. 6011146

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle

; APPLICANT: Abastado, Jean-Pierre

; APPLICANT: Kourilsky, Philippe

; TITLE OF INVENTION: Altered Major Histocompatibility Complex

; NUMBER OF SEQUENCES: 148

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunnet

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/481,985B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/801,818

; FILING DATE: 05-DEC-1991

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 03495.0106-04000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 86:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 42 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Region

; LOCATION: 18..19

; OTHER INFORMATION:

; OTHER INFORMATION: /note= "Xaa is an unidentified

; amino acid residue."

; US-08-481-985B-86

Alignment Scores:

Pred. No.: 97.7 Length: 42

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.92% Indels: 0

DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-481-985B-86 (1-42)

OY 625 ACTTCGATTATCCCTGCC 605
|||||
Db 23 ThrsrAspLeuSerleuPrt 29

RESULT 22
US-08-370-476-86
; Sequence 86, Application US/08370476
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
; APPLICANT: Kourilsky, Philippe
; APPLICANT: Lone, Yu-Chun
; APPLICANT: Ojcius, David
; APPLICANT: Castrouge, Armenda
; TITLE OF INVENTION: Altered Major Histocompatibility Complex
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flinnegan, Henderson, Faradow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/370.476
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117,575
; FILING DATE: 07-SEP-1993
; APPLICATION NUMBER: US 08/072,787
; FILING DATE: 06-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/801,818
; FILING DATE: 05-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473
; FILING DATE: 15-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05243.0001-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 18..19
; OTHER INFORMATION: /note="Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."
US-08-370-476-86

Alignment Scores:
Pred. No.: 97.7
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.92%
DB: 4

Length: 42
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Caps: 0

US-09-817-318-1 (1-780) x US-08-370-476-86 (1-42)
OY 625 ACTTCGATTATCCCTGCC 605
|||||
Db 23 ThrsrAspLeuSerleuPrt 29

RESULT 23
US-09-366-887A-6
; Sequence 6, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366.887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-366-887A-6

Alignment Scores:
Pred. No.: 87.7
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.92%
DB: 4

Length: 97
Matches: 7
Conservative: 0
Mismatch: 0
Indels: 0
Caps: 0

US-09-817-318-1 (1-780) x US-09-366-887A-6 (1-97)
OY 640 TTGTTATTGACGTAACCTCT 620
|||||
Db 10 LeuLeuLeuThrValThrSer 16

RESULT 24
US-09-366-887A-7
; Sequence 7, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366.887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-366-887A-7
Alignment Scores:
Pred. No.: 87.5      Length: 98
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.92%      Indels: 0
DB: 4               Gaps: 0

US-09-817-318-1 (1-780) x US-09-366-887A-7 (1-98)
QY 640 TTGTATTGACAGTACTTCT 620
    |||||
DB 10 leuLeuLeuThrValThrser 16

RESULT 25
US-09-071-035-292
; Sequence 292, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-292

Alignment Scores:
Pred. No.: 86.8      Length: 105
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.86%      Indels: 0
DB: 4               Gaps: 0

US-09-817-318-1 (1-780) x US-09-071-035-292 (1-105)
QY 616 AATCAGAACTACTGTCAATA 636
    |||||
DB 31 AsnGlnLysLeuLeuSerIle 37

US-09-069-023-14
; Sequence 14, Application US/09069023A
; Patent No. 6348573
; GENERAL INFORMATION:
; APPLICANT: Nunez, Gabriel
; APPLICANT: Inohara, Naohiro
; APPLICANT: Koseki, Takeyoshi
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
; TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
; FILE REFERENCE: UM-03333
; CURRENT APPLICATION NUMBER: US/09/069,023A
; CURRENT FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-069-023-14

Alignment Scores:
Pred. No.: 86.6      Length: 107
Score: 7.00         Matches: 7
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.86%      Indels: 0
DB: 4               Gaps: 0

US-09-817-318-1 (1-780) x US-09-069-023-14 (1-107)
QY 281 ACAAGAGGCTCTGTTTACA 301
    |||||
DB 22 ThrLysArgValLeuPheThr 28

RESULT 27
US-09-071-035-290
; Sequence 290, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-035-290

Alignment Scores:

Pred. No.:	84.3	Length:	131
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x US-09-071-035-290 (1-131)

OY 616 AATCAGAGTACTGTCAATA 636
|||||
DB 53 AsnGlnLysLeuLeuSerIle 59

RESULT 28

US-09-134-001C-5047
Sequence 5047, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5047
LENGTH: 206
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5047

Alignment Scores:

Pred. No.:	79.5	Length:	206
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x US-09-134-001C-5047 (1-206)

OY 582 GTCTACTGATAGTCACAT 562
|||||
DB 61 ValLeuThrAspSerGlnHis 67

RESULT 29

US-09-415-522-2
Sequence 2, Application US/09415522A
Patent No. 6291660

GENERAL INFORMATION:

APPLICANT: Gaffney, Thomas
APPLICANT: Wendland, Juergen
APPLICANT: Philippesen, Peter
TITLE OF INVENTION: No. 6291660e1 Fungal Genes Required For No. 6291660ma1 Growth And
FILE REFERENCE: CGC2046
CURRENT APPLICATION NUMBER: US/09/415,522A
CURRENT FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 207
TYPE: PRT

ORGANISM: Ashbya gossypii
US-09-415-522-2

Alignment Scores:

Pred. No.:	79.5	Length:	207
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x US-09-415-522-2 (1-207)

OY 44 ATTTTACTAGCGTGTACGCC 24
|||||
DB 119 IleLeuValGlyCysIlySala 125

RESULT 30

US-09-069-023-12
Sequence 12, Application US/09069023A
Patent No. 6348573

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-09-069-023-12

Alignment Scores:

Pred. No.:	78.9	Length:	219
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x US-09-069-023-12 (1-219)

OY 281 ACAAGAGCGTCTGTTCACA 301
|||||
DB 22 ThrLysArgValLeuPheIhr 28

RESULT 31

US-09-134-001C-5494
Sequence 5494, Application US/09134001C
Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5494
LENGTH: 226
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5494

Alignment Scores:

Pred. No.: 78.6 Length: 226
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 4 Gaps: 0

US-09-817-318-1 (1-780) x US-09-134-001C-5494 (1-226)

QY 542 AAGTCAATGTAATAGATTG 522
|||||

Db 195 ThrValasValasMargLeu 201

RESULT 32

US-08-484-905-65
; Sequence 65, Application US/08484905
; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS-/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905

; FILING DATE: 07-JUNE-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 03495.0106-03000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 326..327
; OTHER INFORMATION: /note= "Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."

US-08-484-905-65

Alignment Scores:

Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x US-08-484-905-65 (1-350)

QY 625 ACTCTGATTATCCGCCCC 605
|||||

Db 331 ThSerAspLeuSerLeuPro 337

RESULT 33

US-08-484-905-67
; Sequence 67, Application US/08484905
; Patent No. 5976551

; GENERAL INFORMATION:

; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre

; TITLE OF INVENTION: An Altered Major Histocompatibility

; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the

; NUMBER OF SEQUENCES: 127

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W., Suite 700

; CITY: Washington

; STATE: D.C.

; ZIP: 20005-3315

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,905

; FILING DATE: 07-JUNE-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/792,473

; FILING DATE: 15-NOV-1991

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.

; REGISTRATION NUMBER: 33,332

; REFERENCE/DOCKET NUMBER: 03495.0106-03000

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400

; TELEFAX: 202-408-4400

; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Region
; LOCATION: 326..327
; OTHER INFORMATION: /note= "Xaa is an unidentified
; OTHER INFORMATION: amino acid residue."

US-08-484-905-67

Alignment Scores:

Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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US-09-817-318-1 (1-780) x US-08-484-905-67 (1-350)
QY 625 ACTTGATTTATCCGCC 605
   |||||||
DB 331 Th1SerAspLeuSerIeuPro 337

RESULT 34
US-08-481-985B--65
: Sequence 65, Application US/08481985B
: Patent No. 6011146
:
: GENERAL INFORMATION:
: APPLICANT: Motiez, Estelle
: APPLICANT: Abastado, Jean-Pierre
: APPLICANT: Kourilsky, Philippe
: TITLE OF INVENTION: Altered Major Histocompatibility Complex
: NUMBER OF SEQUENCES: 148
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fimegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: ZIP: 20005-3315
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,985B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/801,818
: FILING DATE: 05-DEC-1991
: CLASSIFICATION: 435
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/792,473
: FILING DATE: 15-NOV-1991
: CLASSIFICATION: 435
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 03495.0106-04000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-408-4400
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 65:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 326..327
: OTHER INFORMATION: /note="Xaa is an unidentified
: OTHER INFORMATION: amino acid residue."
:
: US-08-481-985B--65

Alignment Scores:
Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-481-985B-65 (1-350)

```

```

      1 625 ACTTCGATTATCCCGCC 605
      2 ||||||||||||||||
      3 db 331 ThrSerAspLeuSerLeuPro 337

RESULT 35
US-08-481-985B-67
: Sequence 67, Application US/08481985B
: Patent No. 6011146
: GENERAL INFORMATION:
: APPLICANT: Mottez, Estelle
: APPLICANT: Abastado, Jean-Pierre
: APPLICANT: Kourilsky, Philippe
: TITLE OF INVENTION: Altered Major Histocompatibility Complex
: NUMBER OF SEQUENCES: 148
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W., Suite 700
: CITY: Washington
: STATE: D.C.
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/481,985B
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/801,818
: FILING DATE: 05-DEC-1991
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/792,473
: FILING DATE: 15-NOV-1991
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 03495.0106-04000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-408-4000
: TELEFAX: 202-408-4400
: INFORMATION FOR SEQ ID NO: 67:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 350 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 326..327
: OTHER INFORMATION: /note="Xaa is an unidentified
: OTHER INFORMATION: amino acid residue."
US-08-481-985B-67

Alignment Scores:
Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-08-481-985B-67 (1-350)

oy 625 ACTTCGATTATCCCGCC 605
|||||
db 331 ThrSerAspLeuSerLeuPro 337

```

RESULT 36
US-08-370-476-65
Sequence 65, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
ADDRESS: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243, 0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 326..327
OTHER INFORMATION: /note="Xaa is an unidentified
OTHER INFORMATION: amino acid residue."
US-08-370-476-65
Alignment Scores:
Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 4 Gaps: 0
US-09-817-318-1 (1-780) x US-08-370-476-65 (1-350)
QY 625 ACTTCGATTATCCCTGCC 605

Db 331 ThrSerAspLeuSerLeuPro 337
|||||
RESULT 37
US-08-370-476-67
Sequence 67, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Motiez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armand
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
ADDRESS: Dunnet
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243, 0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 326..327
OTHER INFORMATION: /note="Xaa is an unidentified
OTHER INFORMATION: amino acid residue."
US-08-370-476-67
Alignment Scores:
Pred. No.: 74.2 Length: 350
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 4 Gaps: 0
US-09-817-318-1 (1-780) x US-08-370-476-67 (1-350)

OY 625 ACTTCGATTATCCCTGCC 605
|||||
DB 331 ThreSerAspLeuSerLeuPro 337

RESULT 38

US-08-153-848-28

; Sequence 28, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESS: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153.848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5759804e1, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 28:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-153-848-28

Alignment Scores:

Pred. No.: 74.1 Length: 355

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.86% Indels: 0

DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-153-848-28 (1-355)

OY 704 TTAATCTCCGCTGTAATA 724

|||||

DB 232 LeuileLeuValValile 238

RESULT 39

US-08-153-848-32

; Sequence 32, Application US/08153848

; Patent No. 5759804

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESS: Bicknell

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/153.848

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,452

; FILING DATE: 17-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 5759804e1, Greta E.

; REGISTRATION NUMBER: 35,302

; REFERENCE/DOCKET NUMBER: 31794

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (312) 474-6300

; TELEFAX: (312) 474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 355 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-153-848-32

Alignment Scores:

Pred. No.: 74.1 Length: 355

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.86% Indels: 0

DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x US-08-153-848-32 (1-355)

OY 704 TTAATCTCCGCTGTAATA 724

|||||

DB 232 LeuileLeuValValile 238

RESULT 40

US-09-299-843A-28

; Sequence 28, Application US/09299843A

; Patent No. 6107475

; GENERAL INFORMATION:

; APPLICANT: Godiska, Ronald

; APPLICANT: Gray, Patrick W.

; APPLICANT: Schweikart, Vicki L.

; TITLE OF INVENTION: No. 6107475e1 Seven Transmembrane Receptors

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

; ADDRESS: Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. UHL
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-28

Alignment Scores:
Pred. No.: 74.1 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-09-299-843A-28 (1-355)

QY 704 TTAATTCCTCGTTGTAATA 724
|||||
DB 232 LeuileuValValIle 238

RESULT 41
US-09-299-843A-32
Sequence 32, Application US/09299843A
Patent No. 6107475
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,843A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/088,337
FILING DATE: 01-JUN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: JILL E. UHL
REGISTRATION NUMBER: 43,213
REFERENCE/DOCKET NUMBER: 27866/32059B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX:
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-299-843A-32

Alignment Scores:
Pred. No.: 74.1 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 3 Gaps: 0

US-09-817-318-1 (1-780) x US-09-299-843A-32 (1-355)

QY 704 TTAATTCCTCGTTGTAATA 724
|||||
DB 232 LeuileuValValIle 238

RESULT 42
US-09-088-337B-28
Sequence 28, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESS: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302

```

: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 355 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-817-318-1 (1-780) x US-09-088-337B-28 (1-355)

Alignment Scores:
Pred. No.: 74.1 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 4 Gaps: 0

QY 704 TTAATCTCCTGCTTGAATA 724
Db 232 LeuileLeuValIle 238

RESULT 43
US-09-088-337B-32
: Sequence 32, Application US/09088337B
: Patent No. 6348574
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: Gray, Patrick W.
: Schweikart, Vicki L.
: TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/088,337B
: FILING DATE: 01-Jun-1998
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/153,848
: FILING DATE: 17-NOV-1993
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 6348574and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 31794
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 355 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
```

```

: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-088-337B-32

Alignment Scores:
Pred. No.: 74.1 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 4 Gaps: 0

US-09-817-318-1 (1-780) x US-09-088-337B-32 (1-355)

QY 704 TTAATCTCCTGCTTGAATA 724
Db 232 LeuileLeuValIle 238

RESULT 44
PCT-US93-11153-28
: Sequence 28, Application PC/TUS9311153
: GENERAL INFORMATION:
: APPLICANT: Godiska, Ronald
: Gray, Patrick W.
: APPLICANT: Schweikart, Vicki L.
: TITLE OF INVENTION: Novel Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/11153
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/977,452
: FILING DATE: 17-NOV-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Noland, Greta E.
: REGISTRATION NUMBER: 35,302
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 474-6300
: TELEFAX: (312) 474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 28:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 355 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US93-11153-28

Alignment Scores:
Pred. No.: 74.1 Length: 355
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x PCT-US93-11153-28 (1-355)
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QY 704 TTAATTCCTCGTGTATATA 724
 |||
 DB 232 LeuileLeuValValIle 238

RESULT 45

PCT-US93-11153-32
 ; Sequence 32, Application PC/TUS9311153
 ; GENERAL INFORMATION:
 ; APPLICANT: Godiska, Ronald
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Schweikart, Vicki L.
 ; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; ADDRESSEE: Bicknell
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US93/11153
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/977,452
 ; FILING DATE: 17-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Noland, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 31794
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US93-11153-32

Alignment Scores:

Pred. No.:	74.1	Length:	355
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	5	Gaps:	0

US-09-817-318-1 (1-780) x PCT-US93-11153-32 (1-355)

QY 704 TTAATTCCTCGTGTATATA 724
 |||
 DB 232 LeuileLeuValValIle 238

Search completed: February 4, 2003, 07:24:18
 Job time : 28.5 secs

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus.n2p model

Run on: February 4, 2003, 07:17:28 : Search time 57.5 Seconds

(without alignments)
5590.148 Million cell updates/sec

Title: US-09-817-318-1

Perfect score: 245

Sequence: 1 aattactgtctctcttaag.....taagggcaaaaaaaaaa 780

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 671580 seqs, 206047115 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1343044

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/c9n2.1/USPTO.spool/US09817318/runat_04022003_071722_6623/app_query.fasta.1.967
-DB=SPTRMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFMT=pio
-NOR=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09817318.ecgn.1.1-88.@runat_04022003_071722_6623 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_MAMMAL:*
6: SP_INVERTEBRATE:*
7: SP_MNC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOZOA:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_RVIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
C 1	11	4.6	350 5 Q8SV97	Q8SV97 encephalito

2	8	3.3	145	16	Q9PM11	Q9PM11 campylobact
3	8	3.3	168	17	Q8ZWK1	Q8ZWK1 pyrobaculum
C 4	8	3.3	235	10	Q65527	Q65527 arabidopsis
C 5	8	3.3	266	16	Q6RYR5	Q6RYR5 deinococcus
C 6	8	3.3	300	5	Q9NH08	Q9NH08 agrotis ips
C 7	8	3.3	311	17	Q8TX17	Q8TX17 methanopyru
9	8	3.3	341	10	Q9S7G2	Q9S7G2 arabidopsis
10	8	3.3	454	10	Q9ZT91	Q9ZT91 arabidopsis
C 11	8	3.3	866	16	Q8UCG6	Q8UCG6 agrobacteri
C 12	8	3.3	963	10	Q9M147	Q9M147 arabidopsis
C 13	8	3.3	1613	16	Q9KRZ1	Q9KRZ1 vibrio chol
C 14	7	2.9	21	8	Q35556	Q35556 pythium oli
C 15	7	2.9	70	12	Q991K5	Q991K5 hepatitis b
C 16	7	2.9	76	17	Q58627	Q58627 methanococ
C 17	7	2.9	90	8	Q9G425	Q9G425 acipenser g
C 18	7	2.9	91	9	Q48470	Q48470 bacterioph
C 19	7	2.9	100	8	Q78856	Q78856 phytophthor
C 20	7	2.9	102	7	Q31193	Q31193 mus musculi
C 21	7	2.9	139	8	Q32919	Q32919 phacelocar
C 22	7	2.9	139	4	Q96DR6	Q96DR6 homo sapien
C 23	7	2.9	146	9	Q34053	Q34053 streptococ
C 24	7	2.9	147	5	Q9XXA6	Q9XXA6 caenorhabdi
C 25	7	2.9	152	8	Q48024	Q48024 candida asp
C 26	7	2.9	152	12	Q9DUM9	Q9DUM9 kaposi's sa
C 27	7	2.9	153	16	Q9A3V4	Q9A3V4 caulobacter
C 28	7	2.9	164	7	Q31156	Q31156 mus musculi
C 29	7	2.9	168	16	Q99R41	Q99R41 staphylococ
C 30	7	2.9	170	8	Q9MR45	Q9MR45 echinococu
C 31	7	2.9	175	10	Q9LS47	Q9LS47 arabidopsis
C 32	7	2.9	175	16	Q9RX34	Q9RX34 plasmodium
C 33	7	2.9	188	5	Q9UON2	Q9UON2 drosophila
C 34	7	2.9	189	9	Q9VYN0	Q9VYN0 drosophila
C 35	7	2.9	193	8	Q8WCU5	Q8WCU5 rhadophus
C 36	7	2.9	196	8	Q36064	Q36064 trichiturus
C 37	7	2.9	207	3	Q989K7	Q989K7 thelmoanaer
C 38	7	2.9	207	3	Q9HF54	Q9HF54 ashbya goss
C 39	7	2.9	211	4	Q9UFW5	Q9UFW5 homo sapien
C 40	7	2.9	219	10	Q9M2H9	Q9M2H9 arabidopsis
C 41	7	2.9	220	15	Q9WK24	Q9WK24 human immun
C 42	7	2.9	220	15	Q9WK23	Q9WK23 human immun
C 43	7	2.9	220	15	Q9WKX1	Q9WKX1 human immun
C 44	7	2.9	220	15	Q9KMW7	Q9KMW7 human immun
C 45	7	2.9	222	16	Q8XFN8	Q8XFN8 salmonella
			224	16	Q99VW2	Q99VW2 staphylococ

ALIGNMENTS

RESULT 1
ID Q8SV97 PRELIMINARY; PRT; 350 AA.
AC Q8SV97;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Hypothetical protein EC006_1070.
GN EC006_1070.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryoniidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarar F.,
RA Prensier G., Barbe V., Peyreillade E., Brotlier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;

"Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi";
RL Nature 414:450-453(2001).
DR EMBL: AL590446; CAD25467.1; -
KW Hypothetical protein. 350 AA; 39829 MW; 239CBF411086C3BA CRC64;
SO SEQUENCE 350 AA; 39829 MW; 239CBF411086C3BA CRC64;

Alignment Scores:
Pred. No.: 0.0276 Length: 350
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.58% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x Q8SV97 (1-350)

QY 336 CTGTCAAAATTCATGAGTCTTGACATTTCT 304
Db 134 LeuSerLysIleHisGluValLeuAspTyrSer 144

RESULT 2

Q9PM11 PRELIMINARY; PRT; 145 AA.
AC Q9PM11;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Putative periplasmic protein.
GN Cj166c.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=NCYC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Kelsey J.M., Churcher C.,
RA Basham D., Chillingworth T., Davies R.M., Felwell T., Holtroyd S.,
RA Jaisels K., Kariyasev A.V., Moule S., Palen M.J., Penn C.W.,
RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA Whitehead S., Barrell B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL: AL139079; CAB73653.1; -
KW Complete proteome.
SO SEQUENCE 145 AA; 16282 MW; 6BE64F3D3BC69BA CRC64;

Alignment Scores:
Pred. No.: 41.1 Length: 145
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x Q9PM11 (1-145)

QY 651 TATGGATTTATAGTGATATAA 674
Db 136 TyrGlyTyrPheIleGlyAspLys 143

RESULT 3

Q8ZWK1 PRELIMINARY; PRT; 168 AA.
AC Q8ZWK1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE P. aerophilum family 550 protein.
GN PAE1755.

OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Filtz-Gibbon S.T., Ladner H., Kim U.-J., Stettler K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL: AE009837; AAL63701.1; -
KW Complete proteome.
SO SEQUENCE 168 AA; 18625 MW; 5A29810C534745FA CRC64;

Alignment Scores:
Pred. No.: 40.1 Length: 168
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 17 Gaps: 0

US-09-817-318-1 (1-780) x Q8ZWK1 (1-168)

QY 698 CATGTTTAACTCCGCTGTA 721
Db 111 HisValIleLeuValVal 118

RESULT 4

Q65527 PRELIMINARY; PRT; 235 AA.
AC Q65527;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Hypothetical 25.9 kDa protein.
GN F4D1.60 OR ATAG32740.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoorge W., Hohnel J.,
RA Meyers H.W., Mayer K.F.X., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoorge W., Meyers H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL022537; CAA18587.1; -
DR EMBL: AL161582; CAB79991.1; -
KW Hypothetical protein.
SO SEQUENCE 235 AA; 25859 MW; CBB9FF0207D292F8 CRC64;

Alignment Scores:
Pred. No.: 38 Length: 235
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x Q65527 (1-235)

```
OY 482 CATAAATCAGTTGGTGATTTTC 459
Db 21 Histyliselerleuglyasppe 28

RESULT 5
O9RYH5 PRELIMINARY: PRT: 266 AA.
AC O9RYH5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Molybdenum ABC transporter, permealase protein, putative.
GN DRA0168.
OS Deinococcus radiodurans.
OC Bacteria: Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Halt D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
DR EMBL: AE001862; AAF12201.1; -.
DR TIGR: DRA0168; -.
DR InterPro: IPR00515; BPD_transp.
DR Pfam: PF00528; BPD_transp; 1.
KM Complete proteome.
SQ SEQUENCE 266 AA; 27799 MW; 673D6AEDADCE9548 CRC64;

Alignment Scores:
Pred. No.: 37.2 Length: 266
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x O9RYH5 (1-266)
OY 646 ATAACTTGTATTGACAGTAAC 623
Db 61 lIethrleuLeuThlvalthr 68

RESULT 6
O9NH08 PRELIMINARY: PRT: 300 AA.
AC O9NH08:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE A1C6 chymotrypsinogen.
OS Agrotis ipsilon (Black cutworm moth).
OC Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
OC Pterygota: Neoptera: Endopterygota: Lepidoptera; Glossata; Ditrysia;
OC Noctuoidea; Noctuidae; Noctuidae; Agrotis.
OX NCBI_TaxID=56364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MIDGUT;
RX MEDLINE=21167524; PubMed=11267902;
RA Mazumdar-Leighton S., Broadway R.M.;
RT "Identification of six chymotrypsin cDNAs from larval midguts of
RT Helicoverpa zea and Agrotis ipsilon feeding on the soybean (Kunitz)
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RT trypsin inhibitor."
RL Insect Biochem. Mol. Biol. 31:633-644(2001).
CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPsin FAMILY.
DR EMBL: AF233730; AAF71517.1; -.
DR HSSP: P00763; IDPO.
DR MEROPS: S01.121; -.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR001254; Ser_protease TRY.
DR Pfam: PF00089; Trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPsin.
DR SMART: SM00020; Tryp_spec; 1.
DR PROSITE: PS50240; TRYPsin_DOM; 1.
DR PROSITE: PS00134; TRYPsin_HIS; UNKNOWN_1.
DR PROSITE: PS00135; TRYPsin_SER; 1.
KW Hydrolyase; Serine protease.
FT CHAIN 61
SQ SEQUENCE 300 AA; 31418 MW; CEDBF8AE2FCC7C6 CRC64;

Alignment Scores:
Pred. No.: 36.5 Length: 300
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x O9NH08 (1-300)
OY 323 ATGAGTCTGTGACTATCTTTTG 300
Db 1 Melysphelenthrlleleu 8

RESULT 7
O8TX17 PRELIMINARY: PRT: 311 AA.
AC O8TX17:
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Phosphate uptake regulator.
GN PHOU OR MK0862.
OS Methanopyrus kandleri.
OC Archaea: Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malikh A.G., Koonin E.V., Kozlovskiy S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010376; AAM02075.1; -.
KM Complete proteome.
SQ SEQUENCE 311 AA; 35909 MW; F3DD03066D43CD09 CRC64;

Alignment Scores:
Pred. No.: 36.3 Length: 311
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x O8TX17 (1-311)
OY 34 GGTGAAGCCTTACTTAAAGA 11
|||||
```

Db 88 GlyValArgProTyrPheLysArg 95

RESULT 8

ID 0957G2 PRELIMINARY; PRT: 341 AA.

AC 0957G2

DT 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)

DE Hypothetical 38.8 kDa protein.

GN T3A5.140 OR F1883.40.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;

OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;

OC eucosids II: Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Bloecher H., Mewes H.W., Lemcke K., Mayer K.F.X., Quetler F.,

RA Salanoubat M.;

RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,

RA Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetler F.,

RA Salanoubat M.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA EU Arabidopsis sequencing project;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AL132979; CAB62445.1; -

DR EMBL: AL049862; CAB42905.1; -

DR InterPro: IPR002495; GI_8.

DR Pfam: PF01501; Glyco_Transf.8; 1.

KW Hypothetical protein; Transferase.

SO SEQUENCE 341 AA; 38774 MW; 96A527DFCFSBP8E CRC64;

Alignment Scores:

Pred. No.:	35.7	Length:	341
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.27%	Indels:	0
DB:	10	Gaps:	0

US-09-817-318-1 (1-780) x 0957G2 (1-341)

QY 98 AGTAGTTATTTATATATATTC 121

Db 3 SerIysPheLeuTyrLeuSer 10

RESULT 9

ID 092T91 PRELIMINARY; PRT: 454 AA.

AC 092T91

DT 01-MAY-1999 (Tremblrel. 10, Created)

DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Elongation factor Tu, mitochondrial precursor.

GN TUFa OR AT4G02930 OR T419.19 OR T5J8.25.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;

OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;

OC eucosids II: Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-CV. COLUMBIA;

RN [2]

RP SEQUENCE FROM N.A.

RA Kuhlman P., Palmer J.D.;

RT "Isolation, expression, and evolution of the gene encoding

RT mitochondrial elongation factor Tu in Arabidopsis thaliana.";

RL Plant Mol. Biol. 23:1057-1070(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;

RX MEDLINE=20083488; PubMed=10617198;

RA Meyer K.F.X., Schueller C., Mambut R., Murphy G., Volckaert G.,

RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,

RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,

RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,

RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,

RA Vos P., Hohenseil J., Zimmermann W., Weller H., Ridley P.,

RA Langham S.-A., McCullagh B., Bihham L., Robben J.,

RA Van der Schueren J., Grymonprez B., Chang Y.-J., Vandenbussche F.,

RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,

RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,

RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke W.,

RA Moilman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,

RA Berner S., Hempel S., Feldpausch M., Lambers S., Van den Daele H.,

RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,

RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,

RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,

RA Pettett A., Rajandream M.-A., Lyne M., Benes V., Reckmann S.,

RA Borkova D., Bloecher H., Scharfe M., Grimm M., Loehert T.-H.,

RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fartmann B., Grandtack K., Dauner D., Hertzl A.,

RA Neumann A., Argitlou A., Vitale D., Liguori R., Piravandi E.,

RA Massenot O., Quigley F., Clapaud G., Muendlein A., Felber R.,

RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,

RA Chefder F., Cooke R., Berger C., Monfort A., Casacuberta E.,

RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,

RA Perez-Perez A., Punnelle B., Bent E., Johnson S., Jacou D., Jesse T.,

RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bieleke C.,

RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,

RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

RA Parnell L., Dedhia N., Gnoj L., Schütz K., Huang E., Spiegel L.,

RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,

RA Stoneking T., Kallick J., Graves T., Harmon G., Edwards J.,

RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,

RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,

RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,

RA Nelson J., Spieth J., Ryan E., Andrews S., Gissel C., Layman D.,

RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,

RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,

RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,

RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,

RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,

RA Chen E., Maria M., Martienssen R., McCombie W.R.;

RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis

RT thaliana.";

RL Nature 402:769-777(1999).

RN [3]

RP SEQUENCE FROM N.A.

RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,

RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,

RA Shekher M., Schütz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE OF 342-454 FROM N.A.

RC STRAIN-CV. COLUMBIA;

RA Cooke R., Landie M., Raynal M., Delseny M.;

RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE OF 296-306, AND SUBCELLULAR LOCATION.

RC TISSUE-LEAF, AND STEM;

RX MEDLINE=21608403; PubMed=11743114;

RA Krufft V., Eubel H., Jaensch L., Werhahn W., Braun H.-P.;

RT "Proteomic approach to identify novel mitochondrial proteins in


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RT Arabidopsis.
RL Plant Physiol. 127:1694-1710(2001).
CC -i- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
DR EMBL: X89227; CAA61511.1; -.
DR EMBL: AF069442; AAC79113.1; -.
DR EMBL: AC004044; AAD15337.1; -.
DR EMBL: AL161495; CAB7778.1; -.
DR EMBL: F14375; CAA23078.1; -.
DR HSSP: P02990; 1EFU.
DR InterPro: IPR004541; EF-Tu.
DR InterPro: IPR004160; EFTU_Cterm.
DR InterPro: IPR004161; EFTU_D2.
DR InterPro: IPR000795; EF-GTPbind.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGACTN_PCT.
DR TIGRFAMS: TIGR00485; EF-Tu; 1.
DR TIGRFAMS: TIGR00231; small_GTP; 1.
DR PROSITE: PS00301; EFACITOR_GTP; 1.
KW Elongation factor; GTP-binding; Protein biosynthesis; Transit peptide;
KW Mitochondrion.
FT TRANSIT 1 51 MITOCHONDRION (POTENTIAL).
FT CHAIN 52 454 ELONGATION FACTOR TU.
FT NP_BIND 74 81 GTP (BY SIMILARITY).
FT NP_BIND 136 140 GTP (BY SIMILARITY).
FT NP_BIND 191 194 GTP (BY SIMILARITY).
FT CONFLICT 1 10 MASVYLRLNPS -> MEPPVDRDIDLAVSSDTIDGMNEFAAA
FT CONFLICT 310 312 (IN REF. 1).
SQ SEQUENCE 454 AA; 49409 MW; B7C2CAlDCC432FDA CRC64;

Alignment Scores:
Pred. No.: 34.1 Length: 454
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x Q9ZT91 (1-454)
QY 587 AAAAGATATTGATTAATGGCAG 610
| | | | | | | | | | | | | | | | | |
Db 323 LysLysLLeuAspAsnGlyGln 330

RESULT 10
Q8UCG6 PRELIMINARY: PRT; 866 AA.
ID Q8UCG6 PRELIMINARY: PRT; 866 AA.
AC Q8UCG6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein Atu2521.
GN Atu2521 OR AGR_C_4580.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,

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RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58."
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
RA Houmlet K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328(2001).
DR EMBL: AE009198; AAL43508.1; -.
DR EMBL: AE008164; AAK88252.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 866 AA; 93876 MW; ID21156AA010EPCE CRC64;

Alignment Scores:
Pred. No.: 30.7 Length: 866
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x Q8UCG6 (1-866)
QY 428 GTTCCTTGCTATATGAACGA 451
| | | | | | | | | | | | | | | | | |
Db 376 ValProLeuProIleIleGluAla 383

RESULT 11
Q9M147 PRELIMINARY: PRT; 963 AA.
ID Q9M147 PRELIMINARY: PRT; 963 AA.
AC Q9M147;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hypothetical 111.4 kDa protein.
GN At4G01210.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL161491; CAB80930.1; -.
DR InterPro: IPR001296; Glycos_Transf_1.
DR Pfam: PF00534; Glycos_Transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 963 AA; 111437 MW; DBB65E093651B184 CRC64;

Alignment Scores:
Pred. No.: 30.1 Length: 963
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 3.33% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x Q9M147 (1-963)

QY 348 AGAAGAGCTACTGTCACAAATT 325

DB 730 Arglysgluserleuserlysile 737

RESULT 12

Q9KRZ1 PRELIMINARY: PRT: 1613 AA.

AC Q9KRZ1; 01-OCT-2000 (TREMblrel. 15, Created)

DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

GN VC1492.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2040683; PubMed=10952301;

RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Olin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio

cholerae.";

RL Nature 406:477-483(2000).

DR EMBL: AE004227; AAF94647.1;

DR TIGR: VC1492;

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 1613 AA; 183558 MW; 58902452A44A6583 CRC64;

Alignment Scores:

Pred. No.: 27.7 Length: 1613
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x Q9KRZ1 (1-1613)

QY 254 AGAGTAAGCTCTGTAAGCTGCA 231

DB 264 ArgValArgSerValLysleuser 271

RESULT 13

Q35556 PRELIMINARY: PRT: 21 AA.

AC Q35556; 01-NOV-1996 (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

GN Hypothetical 2.5 kDa protein.

OS Pythium oligandrum.

OC Mitochondrion.

OC Eukaryota; stramenopiles; Competes; pythiales; Pythiaceae; Pythium.

OX NCBI_TaxID=41045;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=17-L;

RA Martin F.N.;

RT "Linear mitochondrial genome organization in vivo in the genus

Pythium.";

RL Curr. Genet. 27:0-0(1995).

DR EMBL: U28355; AAA70034.1; -
KW Hypothetical protein; Mitochondrion.
SQ SEQUENCE 21 AA; 2491 MW; 883B7AB7A5D4445E CRC64;

Alignment Scores:

Pred. No.: 613 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 8 Gaps: 0

US-09-817-318-1 (1-780) x Q35556 (1-21)

QY 114 TATAAATAACTTACTCTCA 94

DB 14 Tyrlsileasleuser 20

RESULT 14

Q991K5 PRELIMINARY: PRT: 70 AA.

AC Q991K5; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE 01-OCT-2001 (TREMblrel. 18, Last annotation update)

GN Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA Dong J., Cheng J., Wang Q., Shi S., Zhang J., Xia X., Si C.;

RT "HBV quasispecies: preC/C region as example.";

RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.

DR EMBL: AF335737; AAK30081.1;

DR InterPro: IPR02006; Hepatitis-core.

DR Pfam: PF00906; Hepatitis-core; 1.

SQ SEQUENCE 70 AA; 7826 MW; 1460F931A854ABB CRC64;

Alignment Scores:

Pred. No.: 504 Length: 70
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 12 Gaps: 0

US-09-817-318-1 (1-780) x Q991K5 (1-70)

QY 404 TTGTTACTAGTTTCTCTG 424

DB 49 LeuleuthSerpheleuser 55

RESULT 15

Q58627 PRELIMINARY: PRT: 76 AA.

AC Q58627; 01-JUN-1998 (TREMblrel. 06, Created)

DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)

DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)

GN Hypothetical protein MJ1230.

OS Methanococcus jannaschii.

OC Archaea; Euryarchaeota; Methanococci; Methanococcales;

OC Methanococcaceae; Methanococcus.

OX NCBI_TaxID=2190;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 43067;

RX MEDLINE=96337999; PubMed=8688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*.";
 RL Science 273:1058-1073(1996).
 DR EMBL: U67563; AAB99236.1; -.
 DR TIGR: MJ1230; .
 DR InterPro: IPR001052; Rubredoxin.
 DR PROSITE: PS00202; RUBREDOXIN; UNKNOWN_1.
 KW Hypothetical protein: Complete proteome.
 SO SEQUENCE 76 AA; 8903 MW; 2C53E9EABEF0247C CRC64;

Alignment Scores:

Pred. No.:	497	Length:	76
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	17	Gaps:	0

US-09-817-318-1 (1-780) x Q58627 (1-76)

QY 267 AAGTCAATGTGAGAGTAAG 247

Db 58 LysSerIleValLysSerLys 64

RESULT 16

09G425 PRELIMINARY: PRT: 90 AA.

AC 09G425; 01-MAR-2001 (TReMBLrel. 16, Created)

DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Cytochrome b (Fragment).

GN CYTB.

OS Acipenser guldenstadti (Caspian sturgeon) (Russian sturgeon).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;

OC Acipenser.

OX NCBI_TaxID=7902;

RN [1]

RC SEQUENCE FROM N.A.

RA STRAIN=8519L2B024; TISSUE=CAVIAR;

RA Fain S.R., Lemay J.P., Shafer J.A., Hoesch R.M., Hamlin B.C.,

RA Straughan D.J.;

RT "DNA Sequence Identification of Sturgeon Caviars Traveling in World

RT Trade.";

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE

CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY

CC BOUND TO THE PROTEIN (BY SIMILARITY).

CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,

CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CC EMBL: AF308902; AAC47741.1; .

DR InterPro: IPR000179; Cyt_b6.

DR Pfam: PF00033; cytochrome_b_N_1.

DR PROSITE: PS00192; CYTOCHROME_B_HEME; 1.

KW Electron transport; Heme; Mitochondrion; Respiratory chain;

KW Transmembrane.

RT NON_TER 1

FT NON_TER 90

SQ SEQUENCE 90 AA; 10228 MW; 78166B021859BCA7 CRC64;

Alignment Scores:

Pred. No.:	483	Length:	90
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Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	8	Gaps:	0

US-09-817-318-1 (1-780) x Q9G425 (1-90)

QY 780 TTTTGTGCTTGTAC 760

Db 54 PhePhePheCysLeuTyR 60

RESULT 17

048470 PRELIMINARY: PRT: 91 AA.

AC 048470; 01-JUN-1998 (TReMBLrel. 06, Created)

DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Complete nucleotide sequence.

OS Bacteriophage SP1.

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;

OC Lambda-like viruses.

OX NCBI_TaxID=10724;

RN [1]

RP SEQUENCE FROM N.A.

RA Alonso J.C., Luder G., Stege A.C., Chai S., Weise F., Trautner T.A.;

RT "Analysis of the complete nucleotide sequence and functional

RT organization of *Bacillus subtilis* bacteriophage SP1.";

RT Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: X97918; CA65517.1; .

SO SEQUENCE 91 AA; 11090 MW; B326ADE56F21505 CRC64;

Alignment Scores:

Pred. No.:	482	Length:	91
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	9	Gaps:	0

US-09-817-318-1 (1-780) x Q48470 (1-91)

QY 342 GAGTCACTGCAAAATTCAT 322

Db 41 GlusSerLeuSerLysIleHis 47

RESULT 18

078856 PRELIMINARY: PRT: 100 AA.

AC 078856; 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE NADH dehydrogenase subunit 4L.

GN NADH4L.

OS Phytophthora cinnamomi.

OG Mitochondrion.

OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

OC Phytophthora.

OX NCBI_TaxID=4785;

RN [1]

RC SEQUENCE FROM N.A.

RA STRAIN=A2400;

RA MEDLINE=98336900; PubMed=9673029;

RA Dobrowolski M.P., Tommerup I.C., O'Brien P.A.;

RT "Microsatellites in the mitochondrial genome of phytophthora cinnamomi

RT failed to provide highly polymorphic markers for population

RT genetics.";

RT FEMS Microbiol. Lett. 163:243-248(1998).

DR EMBL: AF051359; AAC39493.1; .

DR InterPro: IPR003215; NADH_dh_ubiq1.

DR InterPro: IPR001133; Oxidored_4L.

DR InterPro: IPR003214; Oxidred4L.
 DR Pfam: PF00420; Oxidred_q2; 1.
 DR ProDom: PD000359; Oxidred4L; 1.
 DR ProDom: PD002107; NADH_ch_ubidq; 1.
 KW Mitochondrion.

SEQUENCE 100 AA: 11311 MW: 8909925088B4C4E5 CRC64;

Alignment Scores:

Pred. No.: 475 Length: 100
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: Gaps: 0

US-09-817-318-1 (1-780) x O78856 (1-100)

OY 114 TATAAATTAACCTTACTCTCA 94

DB 93 TylsileasleuLeuSer 99

RESULT 19

O31193 PRELIMINARY: PRT; 102 AA.

AC O31193; PRELIMINARY: PRT; 102 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MHC class I H-2K gene (Q haplotype), clone ph13 (Exons 4-8) mRNA
 GN H2-K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=84068207; PubMed=6689056;
 RA Kress M., Glaros D., Khoury G., Jay G.;
 RT "Alternative RNA splicing in expression of the H-2K gene."
 RL Nature 306:602-604(1983).
 DR EMBL: K01762; AAA39655.1; -.
 DR MGD: MGI:95904; H2-K.
 DR InterPro: IPR003006; IG_MHC.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER
 SQ SEQUENCE 102 AA: 10797 MW: B0D124B792B150C5 CRC64;

Alignment Scores:

Pred. No.: 473 Length: 102
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: Caps: 0

US-09-817-318-1 (1-780) x Q31193 (1-102)

OY 625 ACTTCGATTATTCCTGCC 605

DB 92 ThrsrAspSerLeuPro 98

RESULT 20

O32919 PRELIMINARY: PRT; 129 AA.

AC O32919; PRELIMINARY: PRT; 129 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (Rubisco
 large subunit) (Fragment).
 GN RBCU.
 OS Phaeolocarpus tortuosus.

OG Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
 OC Phaeolocarpaceae; Phaeolocarpus.
 OX NCBI_TaxID=40405;
 RN [1]

RA SEQUENCE FROM N.A.
 RA Frederick S., Hommersand M.H., Freshwater D.W.;
 RT "Erratum: The molecular systematics of some agar- and carrageenan-
 containing marine red algae based on rbcL sequence analysis.";
 RL Hydrobiologia 341:251-251(1996).
 RN [2]

SEQUENCE FROM N.A.

RA Frederick S., Hommersand M.H., Freshwater D.W.;
 RT "The molecular systematics of some agar- and carrageenan-
 containing marine red algae based on rbcL sequence analysis.";
 RL Hydrobiologia 326:125-135(1996).
 CC -1- FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-
 CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
 THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
 REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
 ACTIVE SITE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + O(2) = 3-
 PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE.
 CC -1- CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-
 PHOSPHO-D-GLYCERATE.
 CC -1- SUBUNIT: 8 LARGE CHAINS + 8 SMALL CHAINS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
 DR EMBL: U26826; AAC36421.1; -.
 DR InterPro: IPR000685; Rubisco_large.
 DR Pfam: PF00016; Rubisco_large_N; 1.
 DR Pfam: PF02788; Rubisco_large_C; 1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER
 SQ SEQUENCE 129 AA: 13964 MW: 71FC215D65269B9E CRC64;

Alignment Scores:

Pred. No.: 456 Length: 129
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: Gaps: 0

US-09-817-318-1 (1-780) x Q32919 (1-129)

OY 453 ACTGCTTCGAATTAAGCAAA 433

DB 64 Thrlaserllelecllys 70

RESULT 21

O96DR6 PRELIMINARY: PRT; 139 AA.

ID O96DR6
 AC O96DR6; PRELIMINARY: PRT; 139 AA.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE CSGEF.
 GN SGEF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=PROSTATIC CARCINOMA;
 RA Qi H., Fillion C., Labrie Y., Grenier J., Fournier A., Labrie C.;
 RT "Isolation and androgen regulation of human CSGEF, a splicing variant
 of a new putative member (SGEF) of Dbl family", that maps to 3q25.31.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBD databases.
 DR EMBL: AF415176; AAL27002.1; -.

DR InterPro: IPR001849; PH.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF000018; SH3; 1.
 DR ProDom: PD000066; SH3; 1.
 DR PROSITE: PS50003; PH_DOMAIN; 1.
 DR PROSITE: PS50002; SH3; 1.
 SQ SEQUENCE 139 AA; 15655 MW; 17A9712161A57CC5 CRC64;

Alignment Scores:

Pred. No.: 450 Length: 139
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 4 Gaps: 0

US-09-817-318-1 (1-780) x Q96DR6 (1-139)

OY 526 CTATTACATGACTGACTT 546

Db 12 LeuphethrleuthrValleu 18

RESULT 22

O34053 PRELIMINARY; PRT; 146 AA.
 AC O34053;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ORF22.
 OS Streptococcus thermophilus temperate bacteriophage O1205.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=51534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CNR21205;
 RX MEDLINE=98048466; Pubmed=9387220;
 RA Stanley E., Fitzgerald G.F., Le Marrec C., Fayard B., van Sinderen D.;
 RT "sequence analysis and characterization of phi O1205, a temperate
 bacteriophage infecting Streptococcus thermophilus CNR21205.";
 RL Microbiology 143:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CNR21205;
 RA Stanley E., Fitzgerald G.F., Le Marrec C., Fayard B., van Sinderen D.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U88974; AAC79538.1; -;
 SQ SEQUENCE 146 AA; 16161 MW; CB36026042F8D5BB CRC64;

Alignment Scores:

Pred. No.: 447 Length: 146
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 9 Gaps: 0

US-09-817-318-1 (1-780) x O34053 (1-146)

OY 295 GTTTACAAGAATAGTCAG 315

Db 34 ValTylrlysaTgIleVallys 40

RESULT 23

O9XXA6 PRELIMINARY; PRT; 147 AA.
 AC O9XXA6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE 6R55.2 protein.
 GN 6R55.2.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wallis J.M.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99069613; Pubmed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL: AL031222; CAA20210.1; -;
 SQ SEQUENCE 147 AA; 16637 MW; 2EEDC828C57F95C4 CRC64;

Alignment Scores:

Pred. No.: 446 Length: 147
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x O9XXA6 (1-147)

OY 415 TTTTCTCTGAGTCTCTTT 435

Db 114 PheSerSerValSerSerPhe 120

RESULT 24

O48024 PRELIMINARY; PRT; 152 AA.
 ID O48024;
 AC O48024;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome b (fragment).
 GN CYTB.
 OS Candoia aspera.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Boidea; Boidae;
 OC Candoia.
 OX NCBI_TaxID=51853;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Campbell B.N.;
 RT "Hic Sunt Serpentes - Molecular phylogenetics and the Boide
 (Serpentes: Boidea).";
 RL Thesis (1997), Queen's University, Kingston, Ontario, Canada.
 CC - FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
 CC - COFACTOR: TWO HEME GROUPS (B562 AND B366) WHICH ARE NOT COVALENTLY
 BOUND TO THE PROTEIN (BY SIMILARITY).
 CC - SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CYTOCHROME C1 AND THE RISKE PROTEIN (BY SIMILARITY).
 CC - SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
 DR EMBL: U69752; AAC01786.1; -;
 DR InterPro: IPR000179; Cyt_b_b6.
 DR Pfam: PF00033; cytochrome_b_n; 1.
 KW Electron transport; Heme; Mitochondrion; Respiratory chain;
 FT NON_TER 1 1
 FT NON_TER 152 152
 SQ SEQUENCE 152 AA; 17200 MW; BF19D28F22A49DCB CRC64;

Alignment Scores:

Pred. No.: 444 Length: 152
 Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 8 Gaps: 0

US-09-817-318-1 (1-780) x O48024 (1-152)

OY 646 ATAACTTGTATTGACAGTA 626
 DB 129 IletHrleuLeuThrVal 135

RESULT 25

ID Q9DUM9 PRELIMINARY; PRT; 152 AA.

AC Q9DUM9; PRELIMINARY; PRT; 152 AA.
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE ORF K10.6.
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 ON NCBI_TaxID=37296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20392178; PubMed=10933732;
 RA Lubyova B., Picha P.M.;
 RT "Characterization of a novel human herpesvirus 8-encoded protein,
 RT VIRF-3, that shows homology to viral and cellular interferon
 RT regulatory factors";
 RL J.Virol. 74:8194-8201(2000).
 DR EMBL: AF254765; AAF98389.1;
 SQ SEQUENCE 152 AA; 17801 MW; 9492017B2BCA7076 CRC64;

Alignment Scores:

Pred. No.: 444 Length: 152
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 12 Gaps: 0

US-09-817-318-1 (1-780) x Q9DUM9 (1-152)

OY 492 GCTTTTGAAGAATTGCAC 512
 DB 77 Alaphneglylystlecystthr 83

RESULT 26

ID Q9A3V4 PRELIMINARY; PRT; 153 AA.

AC Q9A3V4; PRELIMINARY; PRT; 153 AA.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein CC3097.
 GN CC3097.
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 ON NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-ATCC 19089 / CB15;
 MEDLINE=21173698; PubMed=11259647;
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Eisen J., Heidelberg J.F., Alley M.R.R., Ohta N., Maddock J.R.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Pladke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL: AE005973; AA025059.1;
 DR TIGR: CC3097;
 KW Hypothetical protein; Complete Proteome.
 SQ SEQUENCE 153 AA; 16852 MW; 7DD975EB3A62A4C CRC64;

Alignment Scores:

Pred. No.: 443 Length: 153
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x Q9A3V4 (1-153)

OY 227 TGTGTGACGCTTACAGACC 247
 DB 144 CysValThrAlaLeuGlnThr 150

RESULT 27

ID Q31156 PRELIMINARY; PRT; 164 AA.

AC Q31156; PRELIMINARY; PRT; 164 AA.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MHC class I H2 antigen gene (Haplotype d) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82150234; PubMed=6278432;
 RA Lalanne J.-L., Breggère F., Delarbre C., Abastado J.-P., Gachelin G.,
 RA Kourilsky P.;
 RT "Comparison of nucleotide sequences of mRNAs belonging to the mouse h-
 RT 2 multigene family";
 RL Nucleic Acids Res. 10:1039-1049(1982).
 DR EMBL: J00395; AAA39579.1;
 DR InterPro: IPR003587; Ig_C1.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00407; IgC1; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 164 AA; 17774 MW; 354250B6C9B3D066 CRC64;

Alignment Scores:

Pred. No.: 438 Length: 164
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 7 Gaps: 0

US-09-817-318-1 (1-780) x Q31156 (1-164)

OY 625 ACTTGTGATTATCCCTGCC 605
 DB 145 ThrSerAspLeuSerLeuPro 151

RESULT 28

ID Q99RA1 PRELIMINARY; PRT; 168 AA.

AC Q99RA1; PRELIMINARY; PRT; 168 AA.
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Truncated-SA protein.
 GN TRUNCATED-SA OR SA2389.
 OS Staphylococcus aureus (strain N315).

```
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus;
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
RA Matsunari H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yanashita A., Oshima K., Furuya K., Yoshino C., Shibata T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003137; BABA3694.1; -.
KW Complete Proteome.
SQ SEQUENCE 168 AA; 18967 MW; D6B388B687BDDB CRC64;

Alignment Scores:
Pred. No.: 436 Length: 168
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x Q9MR41 (1-168)
OY 704 TTATTCCTCGTGTATATA 724
Db 10 LeuLeuLeuValValIle 16

RESULT 29
Q9MR45 PRELIMINARY; PRT; 170 AA.
AC Q9MR45;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ATPase subunit 6.
GN ATP6.
OS Echinococcus vogeli.
OC Mitochondrion.
OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC Cyclophyllidae; Taeniidae; Echinococcus.
OX NCBI_TaxID=6213;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=South America;
RA Fukunaga M., Yokoyama N., Ito A., Nakao M.;
RT "Distribution of Echinococcus multilocularis in Hokkaido, Japan and
RT its geographical migration."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Le T.H., Pearson M.S., Blair D., Dai N., Zhang L.H., McManus D.P.;
RT "Complete mitochondrial genomes confirm the distinctiveness of the
RT horse-dog and sheep-dog strains of Echinococcus granulosus."
RL Parasitology 0:0-0(2002).
DR EMBL: AB027560; BAA95343.1; -.
DR EMBL: AY056612; AAL55466.1; -.
KW Mitochondrion.
SQ SEQUENCE 170 AA; 19726 MW; 948C17E0ED8A6DD2 CRC64;

Alignment Scores:
Pred. No.: 436 Length: 170
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: Gaps: 0
```

```
US-09-817-318-1 (1-780) x Q9MR45 (1-170)
OY 415 TTTTCTCTGTGAGTTCCCTT 435
Db 72 PheSerSerValSerSerPhe 78

RESULT 30
Q9LS47 PRELIMINARY; PRT; 175 AA.
AC Q9LS47;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Calcineurin b subunit (Protein phosphatase 2b regulatory subunit)-like
DE protein (Hypothetical 20.0 kDa protein).
GN At3g18430.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20277480; PubMed=10819329;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:131-135(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Chang E., Dale J.M., Goldsmith A.D.,
RA Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
RA Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamita A., Karlin-Neumann G.,
RA Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M.,
RA Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M.,
RA Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.;
RA Theologis A.;
RT "Full length cDNA of gene At3g18430 (GI:15229640).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamita A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA Davis R.W., Ecker J.R., Theologis A.;
RT "Arabidopsis Open Reading Frame (ORF) Clones."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB026658; BAB01109.1; -.
DR EMBL: AY063789; AAL36096.1; -.
DR EMBL: AY091287; AAM14226.1; -.
DR HSSP: P06705; IAU1.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; EF-hand. 2.
DR ProDom: PD000012; EF-hand. 1.
DR ProSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 20032 MW; B26D6F2ADA26AFED CRC64;

Alignment Scores:
Pred. No.: 433 Length: 175
```

Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 10 Gaps: 0

US-09-817-318-1 (1-780) x Q9LS47 (1-175)

OY 335 AGTGACTCTTTCTAACCTT 355
DB 148 Seraspserphelutheleu 154

RESULT 31

O9RX34 PRELIMINARY; PRT: 175 AA.

AC O9RX34: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
GN DR0481.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RI:
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zaleski C.,
RA Maravosa K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001907; AAF10064.1; -.
DR TIGR: DR0481; -.
KW Hypothetical protein; Complete proteome
SO SEQUENCE 175 AA; 19419 MW; 7B8276EABAD5A890 CRC64;

Alignment Scores:

Pred. No.: 433 Length: 175
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x Q9RX34 (1-175)

OY 701 GTTTAATTCCTCGTGTGTA 721

DB 4 ValLeuLeuLeuValVal 10

RESULT 32

O9U0N2 PRELIMINARY; PRT: 188 AA.

AC O9U0N2: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN MALP3.05.
OS Plasmodium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;

RA Bowman S., Churcher C., Harris B., Harris D., Lawson D., Quail M.,
RA Barrell B.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL031746; CAB63560.1; -.
KW Hypothetical protein
SO SEQUENCE 188 AA; 21896 MW; 7E42C44E9D1C7321 CRC64;

Alignment Scores:

Pred. No.: 428 Length: 188
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 5 Gaps: 0

US-09-817-318-1 (1-780) x Q9U0N2 (1-188)

OY 460 TCAGAGAACTGCTCAAT7AT 440

DB 42 SerGluSncyspneAsnTyr 48

RESULT 33

O9VYNO PRELIMINARY; PRT: 189 AA.

AC O9VYNO: 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
GN CG15927 protein.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;

RA [1]
RN SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle J., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobery C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Polard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svyrkas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003489; AAF48162.1; -;
 DR Flybase: FBgn0030389; CGI5927.
 SO SEQUENCE 189 AA; 22107 MW; 823E42FAF613FA8F CRC64;

Alignment Scores:

Pred. No.:	428	Length:	189
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	5	Gaps:	0

US-09-817-318-1 (1-780) x O9VYN0 (1-189)

OY 769 TTGCGTTTACACCAATATTTA 749
 ||||||||||||||||||
 DB 160 LeuproteinhsgIntyrlcu 166

RESULT 34

O8WCUS PRELIMINARY; PRT; 193 AA.

AC O8WCUS; 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE NADH dehydrogenase subunit II (Fragment).
 GN ND2.
 OS Rhadophis nuchalis.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Colubridae; Natricinae; Rhadophis.
 OX NCBI_TaxID=126483;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21617617; PubMed=11741383;
 RA Alfaro M.E., Arnold S.J.;
 RT "Molecular systematics and evolution of Regina and the thamnophiline
 RT snakes.";
 RL Mol. Phylogenet. Evol. 21:408-423(2001).
 DR EMBL: AF384826; AAL69655.1; -;
 DR InterPro: IPR001750; Oxidored_q1.
 DR Pfam: PF00361; oxidored_q1; 1.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 193
 SO SEQUENCE 193 AA; 21356 MW; 0CD9FD6D73AF929 CRC64;

Alignment Scores:

Pred. No.:	427	Length:	193
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	8	Gaps:	0

US-09-817-318-1 (1-780) x O8WCUS (1-193)

OY 649 AACATACTTGTATTGACA 629
 ||||||||||||||||||
 DB 145 Asn1ethrleuLeuThr 151

RESULT 35

O36064 PRELIMINARY; PRT; 196 AA.

AC O36064; 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Cytochrome b (Fragment).

GN CYTB.

OS Trichurus lepturus.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;

OC Trichuridae; Trichurus.

OX NCBI_TaxID=13733;

RN [1]
 RP SEQUENCE FROM N.A.

RA Block B.A., Finerty J.R., Stewart A.F.R., Kidd J.;

RT "Evolution of endothermy in fish: Mapping physiological traits on a
 RT molecular phylogeny.";

RL Science 0.0-0(1893).

CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN (BY SIMILARITY).

CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

CC EMBL: L1154; AAA32130.1; -;
 CC InterPro: IPR00179; Cyt.b.b6.

DR Pfam: PF00033; cytochrome_b_n.1.
 DR PROSITE: PS00192; CYTOCHROME_B_HEME.1.

KW Electon transport; Heme; Mitochondrion; Respiratory chain;
 KW Transmembrane.

FT NON_TER 1
 FT NON_TER 196
 SO SEQUENCE 196 AA; 22093 MW; 999B30BC62F64930 CRC64;

Alignment Scores:

Pred. No.:	425	Length:	196
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	8	Gaps:	0

US-09-817-318-1 (1-780) x Q36064 (1-196)

OY 780 TTTTNTTTTGGCTTTTAC 760
 ||||||||||||||||||
 DB 44 PhephephecysLeuTyr 50

RESULT 36

O8R9K7 PRELIMINARY; PRT; 197 AA.

AC O8R9K7; 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Predicted enzyme with a TIM-barrel fold.
 GN TTE1600.

OS Thermomanaerobacter tengcongensis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;

OC Thermomanaerobacteriales; Thermomanaerobacteriaceae; Thermomanaerobacter.

OX NCBI_TaxID=119072;

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MB4T / JCM11007;

RX MEDLINE=21992816; PubMed=11997336;

RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
 RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
 RA Tan H., Chen R., Wang J., Yu J., Yang H.;

RT "A complete sequence of *T. tengcongensis* genome.";

RL Genome Res. 12:689-700(2002).
 DR EMBL: AE013115; AAM24804.1; -;
 KW complete proteome.

SO SEQUENCE 197 AA; 22642 MW; AF9FA99A01353CCD CRC64;

Alignment Scores:

Pred. No.:	425	Length:	197
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	16	Gaps:	0

US-09-817-318-1 (1-780) x Q8R9K7 (1-197)

QY 31 GTAAGCCTTACTTTAGAGA 11
|||||

Db 140 ValArgProTyrPheLysArg 146
|||||

RESULT 37

Q9HF54 PRELIMINARY; PRT; 207 AA.

AC Q9HF54; 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE Rho1.
GN RHO1.
OS Ashbya gossypii (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Eremotheciales; Eremothecium.
RN [1]
RX MEDLINE-21100338; PubMed-11156982;
RA Wendland J., Philippson P.;
RT "Cell Polarity and Hyphal Morphogenesis Are Controlled by Multiple Rho-Protein Modules in the Filamentous Ascomycete Ashbya gossypii.";
RT Genetics 157:601-610(2001).
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
DR EMBL; AF210628; AAC41249.1; -.
DR HSP; P06749; 1FTN.
DR InterPro: IPR003578; GTPase_Rho.
DR InterPro: IPR001230; Prenyl_site.
DR InterPro: IPR001806; Ras_tnsfmg.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; Ras; 1.
DR PRINTS: PR00449; RASTRNSFRMG.
DR SMART: SM00174; RHO; 1.
DR TIGR: TIGR00231; small_GTP; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
KW GTP-binding; Lipoprotein; Prenylation.
SQ SEQUENCE 207 AA; 23045 MW; 0A71F6A434C33B3A CRC64;

Alignment Scores:

Pred. No.:	422	Length:	207
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	3	Gaps:	0

US-09-817-318-1 (1-780) x Q9HF54 (1-207)

QY 44 ATTTAGTAGGTGTAAGGCC 24
|||||

Db 119 IleLeuValGlyCysLysAla 125
|||||

RESULT 38

Q9UFW5 PRELIMINARY; PRT; 211 AA.

AC Q9UFW5; 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE Hypothetical 24.0 kDa protein (Fragment).
GN DKFZP434D146.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RX MEDLINE-9606;
RA Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann S.;
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL117429; CAB55918.1; -.
DR InterPro: IPR001849; PH.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRODOM: PD000066; SH3; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00326; SH3; 1.
DR PROSITE: PS50003; PH_DOMAIN; 1.
DR PROSITE: PS50002; SH3; 1.
KW Hypothetical protein; SH3 domain.
FT NON_TER 1
SQ SEQUENCE 211 AA; 23985 MW; B85D722F4E6AE2B0 CRC64;

Alignment Scores:

Pred. No.:	420	Length:	211
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	4	Gaps:	0

US-09-817-318-1 (1-780) x Q9UFW5 (1-211)

QY 526 GTATTACATGCTGACTT 546
|||||

Db 84 LeuphethLeuthrValieu 90
|||||

RESULT 39

Q9M2H9 PRELIMINARY; PRT; 219 AA.

ID Q9M2H9
AC Q9M2H9;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE Hypothetical 24.6 kDa protein.
GN F9924.280.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
RN [1]
RX MEDLINE-3702;
RA D'Angelo M., Vezzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL137081; CAB68175.1; -.
DR PROSITE: PS50003; PH_DOMAIN; 1.
KW Hypothetical protein.
SQ SEQUENCE 219 AA; 24620 MW; A79263FD56D43BC0 CRC64;

Alignment Scores:

Pred. No.:	418	Length:	219
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	10	Gaps:	0

US-09-817-318-1 (1-780) x Q9WK24 (1-219)

OY 760 GTAAGCGCAAAAAAAAAAAAAA 780

Db 164 VALLYSALALysLYsLYsLYs 170

RESULT 40

O9WK24 PRELIMINARY: PRT: 220 AA.

AC Q9WK24; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Reverse transcriptase (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=260PT15W8C; PubMed=10681363;

RA Demeter L.M., Shafer R.W., Meehan P.M., Holden-Wiltse J., Fischl M.A.,

RT Freimuth W.W., Para M.F., Reichman R.C.;

RT "Delavirdine susceptibility and associated reverse transcriptase

RT mutations in a phase I/II trial of delavirdine monotherapy (ACTG

RT 260)."

RL Antimicrob. Agents Chemother. 44:794-797(2000).

DR EMBL: AF090478; AAC80472.1; -

DR InterPro: IPR000477; RVTse.

DR Pfam: PF00078; rvt; 1.

KW RNA-directed DNA polymerase.

FT NON_TER 1 1

FT NON_TER 220 220

SO SEQUENCE 220 AA; 25790 MW; EDFDC39B0721EC12 CRC64;

Alignment Scores:

Pred. No.: 418 Length: 220
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 15 Gaps: 0

US-09-817-318-1 (1-780) x Q9WK24 (1-220)

OY 135 TATGAACATCTTGATATAA 115

Db 207 TyrgluehHisLeuAspLys 213

RESULT 41

O9WK23 PRELIMINARY: PRT: 220 AA.

AC Q9WK23; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Reverse transcriptase (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=260PT15W8P; PubMed=10681363;

RA Demeter L.M., Shafer R.W., Meehan P.M., Holden-Wiltse J., Fischl M.A.,

RT Freimuth W.W., Para M.F., Reichman R.C.;

RT "Delavirdine susceptibility and associated reverse transcriptase

RT mutations in a phase I/II trial of delavirdine monotherapy (ACTG

RT patients in a phase I/II trial of delavirdine monotherapy (ACTG

RT 260)."

RL Antimicrob. Agents Chemother. 44:794-797(2000).

DR EMBL: AF090479; AAC80473.1; -

DR InterPro: IPR000477; RVTse.

DR Pfam: PF00078; rvt; 1.

KW RNA-directed DNA polymerase.

FT NON_TER 1 1

FT NON_TER 220 220

SO SEQUENCE 220 AA; 25753 MW; 770EB197D9F232E CRC64;

Alignment Scores:

Pred. No.: 418 Length: 220
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 15 Gaps: 0

US-09-817-318-1 (1-780) x Q9WK23 (1-220)

OY 135 TATGAACATCTTGATATAA 115

Db 207 TyrgluehHisLeuAspLys 213

RESULT 42

O9WKX1 PRELIMINARY: PRT: 220 AA.

AC Q9WKX1; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Reverse transcriptase (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=260PT26W8P; PubMed=10681363;

RA Demeter L.M., Shafer R.W., Meehan P.M., Holden-Wiltse J., Fischl M.A.,

RT Freimuth W.W., Para M.F., Reichman R.C.;

RT "Delavirdine susceptibility and associated reverse transcriptase

RT mutations in a phase I/II trial of delavirdine monotherapy (ACTG

RT patients in a phase I/II trial of delavirdine monotherapy (ACTG

RT 260)."

RL Antimicrob. Agents Chemother. 44:794-797(2000).

DR EMBL: AF090506; AAC80500.1; -

DR InterPro: IPR000477; RVTse.

DR Pfam: PF00078; rvt; 1.

KW RNA-directed DNA polymerase.

FT NON_TER 1 1

FT NON_TER 220 220

SO SEQUENCE 220 AA; 25750 MW; BC161482A7AZCE0A CRC64;

Alignment Scores:

Pred. No.: 418 Length: 220
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 15 Gaps: 0

US-09-817-318-1 (1-780) x Q9WKX1 (1-220)

OY 135 TATGAACATCTTGATATAA 115

Db 207 TyrgluehHisLeuAspLys 213

RESULT 43

O9WKW7 PRELIMINARY: PRT: 220 AA.

ID Q9WKW7; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

GN Reverse transcriptase (Fragment).

OS Human immunodeficiency virus type 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=260PT15W8P; PubMed=10681363;

RA Demeter L.M., Shafer R.W., Meehan P.M., Holden-Wiltse J., Fischl M.A.,

RT Freimuth W.W., Para M.F., Reichman R.C.;

RT "Delavirdine susceptibility and associated reverse transcriptase

RT mutations in a phase I/II trial of delavirdine monotherapy (ACTG

RT patients in a phase I/II trial of delavirdine monotherapy (ACTG

RT 260)."

RL Antimicrob. Agents Chemother. 44:794-797(2000).

DR EMBL: AF090506; AAC80500.1; -

DR InterPro: IPR000477; RVTse.

DR Pfam: PF00078; rvt; 1.

KW RNA-directed DNA polymerase.

FT NON_TER 1 1

FT NON_TER 220 220

SO SEQUENCE 220 AA; 25750 MW; BC161482A7AZCE0A CRC64;

DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Reverse transcriptase (Fragment).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 NC NCBL_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-260PT28W8C;
 RA MEDLINE-20145414; PubMed-10681363;
 RA Demeter L.M., Shaffer R.W., Meenan P.M., Holden-Wiltse J., Fischl M.A.,
 RA Freimuth W.W., Para M.F., Reichman R.C.;
 RT "Delavirdine susceptibilities and associated reverse transcriptase
 RT mutations in human immunodeficiency virus type 1 isolates from
 RT patients in a phase I/II trial of delavirdine monotherapy (ACTG
 RT 260).";
 RL Antimicrob. Agents Chemother. 44:794-797(2000).
 DR EMBL; AF090510; AAC80504.1; -;
 DR InterPro: IPR000477; RVTse.
 DR Pfam: PF000078; rvt.1.
 DR RNA-directed DNA polymerase.
 KM NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 220 AA; 25751 MW; 56CDA18384B026B8 CRC64;

Alignment Scores:

Pred. No.:	418	Length:	220
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	15	Gaps:	0

US-09-817-318-1 (1-780) x Q9KFW7 (1-220)

QY 135 TATGAACCTTGGATATAA 115

Db 207 TyrgluuhtsluAspLys 213

RESULT 44

Q8XFN8 PRELIMINARY; PRT; 222 AA.
 AC Q8XFN8;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE GTP cyclohydrolase I (EC 3.5.4.16).
 GN FOIE OR STM2193 OR STY2427.
 OS Salmonella typhimurium, and
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 NC NCBL_TaxID=602; 601;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC SPECIES-S typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RA MEDLINE-21534948; PubMed-11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewl N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S typhi; STRAIN-CT18;
 RA MEDLINE-21534947; PubMed-11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., White N., White N., Farrar J.,
 RA Rietveld T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen J.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Skellern M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 DR EMBL; AF008797; AA121097.1; -;
 DR EMBL; AL627273; CAD02575.1; -;
 DR InterPro: IPR001474; GTP_cyclohydrol.
 DR Pfam: PF01227; GTP_cyclohydrol.1.
 DR ProDom: PD003330; GTP_cyclohydrol.1.
 DR TRFAMS: TRFR0063; foie.1.
 DR PROSITE: PS00859; GTP_CYCLOHYDROL_1_1; 1.
 DR PROSITE: PS00860; GTP_CYCLOHYDROL_1_2; 1.
 KM Hydrolase; Complete proteome.
 SQ SEQUENCE 222 AA; 24770 MW; 906EB3877D1F444E CRC64;

Alignment Scores:

Pred. No.:	417	Length:	222
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	16	Gaps:	0

US-09-817-318-1 (1-780) x Q8XFN8 (1-222)

QY 233 ACAGCTTACAGACCTTACTC 253

Db 161 Thralaenclnhrleu 167

RESULT 45

Q99VW2 PRELIMINARY; PRT; 224 AA.
 AC Q99VW2;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Hypothetical protein SA0614.
 GN SA0614.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus;
 NC NCBL_TaxID=158679;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE-21311952; PubMed-11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino J., Ito T., Kanamori M.,
 RA Matsunaru H., Maruyama A., Murakami H., Hoshiyama A., Mizutani Y.,
 RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 RA Hirakawa H., Kuhara S., Goto S., Yabuuchi J., Kanehisa M.,
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
 RA Ogasawara N., Hayashi H., Hiramatsu K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 CC -1- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
 CC REGULATORY COMPONENTS OF SENSOR TRANSDUCTION SYSTEMS.
 CC -1- SIMILARITY: TO BACTERIAL REGULATORY PROTEINS INVOLVED IN SIGNAL
 CC TRANSDUCTION.
 DR EMBL; AP003131; BAB41847.1; -;
 DR HSSP: P08402; 1B00.
 DR InterPro: IPR001789; Response_reg.
 DR InterPro: IPR001867; Trans_reg_C.
 DR Pfam: PF00072; response_reg.1.
 DR Pfam: PF00486; trans_reg_C.1.
 DR ProDom: PD000039; Response_reg.1.
 DR ProDom: PD000329; Trans_reg_C.1.
 DR SMART: SM00448; REC; 1.

KW DNA-binding; Phosphorylation; Sensory transduction;
KW Transcription regulation; Hypothetical protein; Complete proteome.
SQ SEQUENCE 224 AA; 26066 MW; 4A636CBAA6FAD233 CRC64;

Alignment Scores:

Pred. No.:	416	Length:	224
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	16	Gaps:	0

US-09-817-318-1 (1-780) x Q99VW2 (1-224)

QY 542 ACAGTCAATGTAATAGATTG 522

DB 193 ThrValAsnValAsnArgLeu 199

Search completed: February 4, 2003, 07:20:21
Job time : 67.5 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 4, 2003, 07:17:29; Search time 43.5 seconds

(Without alignments)
4778.643 Million cell updates/sec

Title: US-09-817-318-1

Perfect score: 245
Sequence: 1 aattactgtctctcttaag.....taagcgcaaaaaaaaaa 780

Scoring table:

OLIGO
Xgapop 60.0, Xgapext 60.0
Ygapop 60.0, Ygapext 60.0
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 908470 segs, 133250620 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1687582

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=framer_n2p_model -DEV=xlp
-O=cgnt2_1/USPTO.spool/US09817318/runat_04022003_071721_6604/app-query.fasta.1.967
-DB=A.geneseq-101002 -OPM=fastan -SOFIT=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTFM=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09817318.@CGN_1.1.30.@runat_04022003_071721_6604 -NCPU=6 -ICPU=3
-NO_XLIFY -NO_MMAP -LARGEOUT -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WANT_TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6 -Fgapext=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database:

A.Geneseq.101002: *
1: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1980.DAT: *
2: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1981.DAT: *
3: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1982.DAT: *
4: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1983.DAT: *
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11: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1990.DAT: *
12: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1991.DAT: *
13: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1992.DAT: *
14: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1993.DAT: *
15: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1994.DAT: *
16: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1995.DAT: *
17: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1996.DAT: *
18: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1997.DAT: *
19: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1998.DAT: *
20: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA1999.DAT: *
21: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA2000.DAT: *
22: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA2001.DAT: *
23: /SIDS2/gcgdata/geneseq/geneseq_emb1/AA2002.DAT: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	3.3	51	22	ABG20710	Novel human diagno
2	8	3.3	55	22	ABG07001	Novel human diagno
3	8	3.3	93	22	AAH67296	Human immune/haema
4	8	3.3	341	23	ABH92615	Heridically activ
5	8	3.3	397	21	AAH29847	Arabidopsis thalia
6	8	3.3	397	21	AAH29847	Arabidopsis thalia
7	8	3.3	454	21	AAH29846	Arabidopsis thalia
8	8	3.3	454	21	AAH29846	Arabidopsis thalia
9	8	3.3	455	21	AAH29845	Arabidopsis thalia
10	8	3.3	470	21	AAH29845	Arabidopsis thalia
11	8	3.3	593	21	AAH29845	Arabidopsis thalia
12	8	3.3	593	21	AAH29845	Arabidopsis thalia
13	8	3.3	645	21	AAH29845	Arabidopsis thalia
14	8	3.3	645	21	AAH29845	Arabidopsis thalia
15	8	3.3	716	21	AAH29845	Arabidopsis thalia
16	8	3.3	717	21	AAH29845	Arabidopsis thalia
17	7	2.9	21	16	AAH29845	Peptide enhancer o
18	7	2.9	21	16	AAH29845	Synthetic anti-neo
19	7	2.9	21	16	AAH29845	Tryptic digestion
20	7	2.9	21	16	AAH29845	Amphipathic peptid
21	7	2.9	21	17	AAH29845	Lytic peptide used
22	7	2.9	21	17	AAH29845	Synthetic lytic pe
23	7	2.9	21	19	AAH29845	Synthetic lysine-r
24	7	2.9	28	22	ABG27285	Novel human diagno
25	7	2.9	38	21	AAH29845	Murine class I mol
26	7	2.9	38	21	AAH29845	Murine class I mol
27	7	2.9	38	22	AAH29845	Murine class I pr
28	7	2.9	42	21	AAH29845	Murine class I mol
29	7	2.9	42	21	AAH29845	Murine class I mol
30	7	2.9	42	22	AAH29845	Human immune/haema
31	7	2.9	42	22	AAH29845	Murine class I pr
32	7	2.9	46	22	AAH29845	Novel human diagno
33	7	2.9	71	22	AAH29845	Human prostate can
34	7	2.9	71	22	AAH29845	Human prostate can
35	7	2.9	87	17	AAH29845	Protein reactive w
36	7	2.9	87	21	AAH29845	Human secreted pro
37	7	2.9	88	20	AAH29845	Human 5' EST seque
38	7	2.9	88	22	AAH29845	Human polypeptide
39	7	2.9	91	23	AAH29845	Human ORFX protein
40	7	2.9	94	21	AAH29845	Zea mays protein f
41	7	2.9	97	23	AAH29845	Murine ectoxin pol
42	7	2.9	98	23	AAH29845	Murine ectoxin pol
43	7	2.9	99	22	AAH29845	Protonibacterium
44	7	2.9	100	22	AAH29845	Human polypeptide
45	7	2.9	104	23	ABP31587	Human ORF560 prote

ALIGNMENTS

RESULT 1
ID ABG20710 standard; Protein: 51 AA.

AC ABG20710;
DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #20701.

OS Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

XX 11-OCT-2001.
XX

PF 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Iliu C, Tang YT;
XX
XX WPI: 2001-639362/73.
DR N-PSDB: AAS84897.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
PS Claim 20; SEQ ID No 51069; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 51 AA;
SQ
Alignment Scores:
Pred. No.: 29.2 Length: 51
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 22 Gaps: 0
US-09-817-318-1 (1-780) x ABG20710 (1-51)
OY 448 AGCAGTCTCTGAAATCACCAGAA 471
DB 33 SerSerSerLeuYSerProLys 40
RESULT 2
ABG07001
ID ABG07001 standard; Protein: 55 AA.
XX
XX ABG07001;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #6992.
DE
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensics;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX WO200175067-A2.
PN

XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US08631.
PF
XX
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
PA
PI Drmanac RT, Iliu C, Tang YT;
XX
XX WPI: 2001-639362/73.
DR N-PSDB: AAS11188.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
PS Claim 20; SEQ ID No 37360; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 55 AA;
SQ
Alignment Scores:
Pred. No.: 29.1 Length: 55
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 22 Gaps: 0
US-09-817-318-1 (1-780) x ABG07001 (1-55)
OY 193 AAATTACATTTATTCATTTT 170
DB 29 LysLeuThrPheYSerPhePhe 36
RESULT 3
AAM87296
ID AAM87296 standard; Protein: 93 AA.
XX
XX AAM87296;
AC
XX
XX 07-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen SEQ ID NO:14889.
DE
XX
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.
XX
XX

OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
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PR 14-AUG-2000; 2000US-0224518.
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PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 08-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.

PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239933.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249246.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 01-DEC-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251031.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
PR 05-JAN-2001; 2001US-02559678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.

PI	Rosen CA,	Barash SC,	Ruben SM,	
XX				
DR	WPI: 2001-483426/52.			
DR	N-PSDB: AAK60077.			
XX				
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -			
XX				
PS	Claim 11: SEQ ID NO 14889; 3071pp + Sequence Listing; English.			
XX				
CC	AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (II) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patient's own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.			
CC				
XX				
XX	Sequence	93 AA;		
XX				
XX	Alignment Scores:			
XX	Pred. No.:	28	Length:	93
XX	Score:	8.00	Matches:	8
XX	Percent Similarity:	100.00%	Conservative:	0
XX	Best Local Similarity:	100.00%	Mismatches:	0
XX	Query Match:	3.33%	Indels:	0
XX	DB:	22	Gaps:	0
XX				
XX	US-09-817-318-1 (1-780) x AAM87296 (1-93)			
XX				
OY	634 TTGACAGTAACCTGCGATTATCC	611		
DB				
DB	71 LeuThrValThrSerAspLeuSer	78		
XX				
XX	RESULT 4			
XX	ABB92615			
XX	ID ABB92615 standard; Protein; 341 AA.			
XX	ABB92615:			
XX				
XX	31-MAY-2002 (first entry)			
XX				
XX	Herbicideally active polypeptide SEQ ID NO 1826.			
XX				
XX	Herbicideal; plant; agriculture; herbicide.			
XX				
XX	Arabidopsis thaliana.			
XX				
XX	WO200210210-A2.			
XX				
XX	07-FEB-2002.			
XX				
XX	28-AUG-2001; 2001WO-EP09892.			
XX				
XX	28-AUG-2001; 2001WO-EP09892.			
XX				
XX	(FARB) BAYER AG.			
XX				
XX	Tietjen K, Weidner M;			
XX				
XX	WPI: 2002-269010/31.			

XX	Identifying plant target proteins for herbicidally active compounds,
PT	comprising aligning and comparing nucleic acid or amino acid sequences
PT	from plant with nucleic acid or amino acid sequences from non-plant
PT	organisms -
PS	Claim 5; SEQ ID NO 1826; 261bp + Sequence Listing; English.
XX	
CC	The invention relates to identifying target proteins
CC	(ABB90790-ABB94016) for herbicidally active compounds, comprising
CC	aligning and comparing nucleic acid or amino acid sequences from plant
CC	with nucleic acid or amino acid sequences from non-plant organisms using
CC	suitable search parameters, where plant sequences having an E-value
CC	greater by a factor of 3 than the E-value of most similar non-plant
CC	sequences are selected. The polypeptides or nucleic acids encoding them
CC	are useful for identifying modulators. The identified modulators are
CC	useful as herbicides.
XX	
XX	Sequence 341 AA;
XX	
XX	Alignment Scores:
XX	Pred. No.: 25.7 Length: 341
XX	Score: 8.00 Matches: 8
XX	Percent Similarity: 100.00% Conservative: 0
XX	Best Local Similarity: 100.00% Mismatches: 0
XX	Query Match: 3.27% Indels: 0
XX	DB: 23 Gaps: 0
XX	
XX	US-09-817-318-1 (1-780) x ABB92615 (1-341)
XX	
OY	98 AGTAGTTATTTATTTATTTATCC 121
XX	
DB	3 SerLysPheIleLeuTyrLeuSer 10
XX	
XX	RESULT 5
ID	AAG29847
XX	AAG29847 standard; Protein: 397 AA.
XX	
AC	AAG29847;
XX	
XX	17-Oct-2000 (first entry)
DE	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 35580.
XX	
XX	Protein identification: signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter.
XX	termination sequence.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
XX	06-SEP-2000.
XX	
XX	25-FEB-2000; 2000EP-0301439.
XX	
XX	25-FEB-1999; 990S-0121825.
PR	05-MAR-1999; 990S-0123180.
PR	09-MAR-1999; 990S-0123548.
PR	23-MAR-1999; 990S-0125788.
PR	25-MAR-1999; 990S-0126264.
PR	29-MAR-1999; 990S-0126785.
PR	01-APR-1999; 990S-0127462.
PR	06-APR-1999; 990S-0128234.
PR	08-APR-1999; 990S-0128714.
PR	16-APR-1999; 990S-0129845.
PR	19-APR-1999; 990S-0130077.
PR	21-APR-1999; 990S-0130449.
PR	23-APR-1999; 990S-0130510.
PR	28-APR-1999; 990S-0130891.
PR	30-APR-1999; 990S-0131449.
PR	30-APR-1999; 990S-0132048.
PR	30-APR-1999; 990S-0132407.

PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 03-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137724.
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PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139753.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 03-AUG-1999; 99US-0146389.
PR 04-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.

PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
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ID AAC34905 standard; Protein: 397 AA.

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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 42549.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

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XX EP1033405-A2.

XX 06-SEP-2000.

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Alignment Scores:
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US-09-817-318-1 (1-780) x AAG29846 (1-454)

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Db 323 LysLysIleuaspasnGlyGln 330

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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
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PD 06-SEP-2000.
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US-09-817-318-1 (1-780) x AAG34904 (1-454)

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XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 35578.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

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US-09-817-318-1 (1-780) x AAG29845 (1-455)

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Db 324 LyslysilLeuaspasnGlyGln 331

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XX 18-OCT-2000 (first entry)
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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Alignment Scores:
Pred. NO.: 25.1
Score: 8.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
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DB: 21
Gaps: 0

US-09-817-318-1 (1-780) x AAG34903 (1-470)

Oy 587 AAAAGATATAGATTAATGGCAG 610
Db 339 LysLysIleLeuAspAsnGlyGln 346

RESULT 11
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ID AAG23149 standard; Protein: 593 AA.
XX AC AAG23149;
XX DT 17-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 26348.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
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Alignment Scores:

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Query Match:	3.33%	Indels:	0
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US-09-817-318-1 (1-780) x AAG23149 (1-593)

QY 482 CATTAATCAGTTTGGTGATTTTC 459

Db 398 HislySileserleuGlyAspPhe 405

RESULT 12

AAG60457
ID AAG60457 standard; Protein: 593 AA.

AC AAG60457;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 78307.

KM Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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Alignment Scores:
Pred. No.: 24.7
Score: 8.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.33%
DB: 21
Gaps: 0

US-09-817-318-1 (1-780) x AAG60457 (1-593)

QY 482 CATAAATCAGTTGGGATTTTC 459
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Db 398 HsLysIleSerIeuGlyasphe 405

RESULT 13
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ID AAG23148 standard; Protein; 645 AA.
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AC AAG23148;
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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 26347.
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX 06-SEP-2000.
PD XX
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PF 25-FEB-2000; 2000EP-0301439.
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
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KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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PR 07-SEP-1999; 990S-0152363.
PR 10-SEP-1999; 990S-0153070.
PR 13-SEP-1999; 990S-0153758.
PR 15-SEP-1999; 990S-0154018.
PR 16-SEP-1999; 990S-0154039.
PR 20-SEP-1999; 990S-0154779.
PR 22-SEP-1999; 990S-0155139.
PR 23-SEP-1999; 990S-0155486.
PR 24-SEP-1999; 990S-0155659.
PR 28-SEP-1999; 990S-0156458.
PR 29-SEP-1999; 990S-0156596.
PR 04-OCT-1999; 990S-0157117.
PR 05-OCT-1999; 990S-0157753.
PR 06-OCT-1999; 990S-0157865.
PR 07-OCT-1999; 990S-0158029.
PR 08-OCT-1999; 990S-0158222.
PR 12-OCT-1999; 990S-0158369.
PR 13-OCT-1999; 990S-0159293.
PR 13-OCT-1999; 990S-0159294.
PR 13-OCT-1999; 990S-0159295.
PR 14-OCT-1999; 990S-0159329.
PR 14-OCT-1999; 990S-0159330.
PR 14-OCT-1999; 990S-0159331.
PR 14-OCT-1999; 990S-0159637.
PR 14-OCT-1999; 990S-0159638.
PR 18-OCT-1999; 990S-0159584.
PR 21-OCT-1999; 990S-0160741.
PR 21-OCT-1999; 990S-0160747.
PR 21-OCT-1999; 990S-0160766.
PR 21-OCT-1999; 990S-0160770.
PR 21-OCT-1999; 990S-0160814.
PR 21-OCT-1999; 990S-0160815.
PR 22-OCT-1999; 990S-0160980.
PR 22-OCT-1999; 990S-0160981.
PR 22-OCT-1999; 990S-0160989.
PR 25-OCT-1999; 990S-0161404.
PR 25-OCT-1999; 990S-0161405.
PR 25-OCT-1999; 990S-0161406.
PR 26-OCT-1999; 990S-0161359.
PR 26-OCT-1999; 990S-0161360.
PR 26-OCT-1999; 990S-0161361.
PR 28-OCT-1999; 990S-0161920.
PR 28-OCT-1999; 990S-0161992.
PR 28-OCT-1999; 990S-0161993.
PR 29-OCT-1999; 990S-0162142.

Alignment Scores:
Pred. No.:

24.4

Length:

716

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 21 Gaps: 0

US-09-817-318-1 (1-780) x AAG60455 (1-716)

OY 482 CATAAATCAGTTGGGTGATTTC 459
|||||
Db 521 HistylisSerLeuGlyAspPhe 528

RESULT 16
AAG23147
ID AAG23147 standard; Protein: 717 AA.
XX AAG23147;
AC AAG23147;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26346.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0131449.
PR 30-APR-1999; 9905-0132048.
PR 04-MAY-1999; 9905-0132407.
PR 05-MAY-1999; 9905-0132484.
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PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
PR 11-MAY-1999; 9905-0132486.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134370.
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PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136382.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
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PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.

PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138540.
PR 10-JUN-1999; 9905-0138847.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
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PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139859.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
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PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
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PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144884.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 26-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0146389.
PR 04-AUG-1999; 9905-0147208.
PR 04-AUG-1999; 9905-0147204.
PR 05-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.

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PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157863.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Alignment Scores:
Pred. No.:
Score:
Percent Similarity:

24.4
8.00
100.00%

Length:
Matches:
Conservative:

717
8
0

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Best Local Similarity: 100.00%
Query Match: 3.33%
DB: 21
Mismatches: 0
Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x AAR84158 (1-717)

QY 482 CATMAATCAGTTGGGTGATTTTC 459
|||||
DB 522 HSLYSILSERLLEUGLYASPHE 529

RESULT 17
AAR84158
ID AAR84158 standard; peptide; 21 AA.
XX
AC AAR84158;
XX
DT 06-JUN-1996 (first entry)
XX
DE Peptide enhancer of fibroblast and keratinocyte proliferation.
XX
KW amphipathic peptide; enhance; fibroblast; keratinocyte; proliferation;
KW wound healing; defensin; antimicrobial.
XX
OS Synthetic.
XX
PN WO9528832-A1.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US04718.
XX
PR 20-APR-1994; 94US-0231730.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
DR WPI; 1995-382791/49.
XX
PT Use of amphipathic peptide(s) - for enhancing fibroblast and
PT keratinocyte proliferation to promote wound healing in a mammal
XX
XX
PS Claim 7; Page 52-53; 64pp; English.
XX
CC AAR84128-73 are amphipathic peptides which are able to stimulate the
CC proliferative growth of fibroblasts and epithelial cells such as
CC keratinocytes, hence enhancing wound healing in mammalian subjects.
CC The peptides concomitantly have antimicrobial efficacy, against
CC microbial species including those which cause or otherwise mediate
CC sepsis and wound infection.
XX
SQ Sequence 21 AA;

Alignment Scores:
Pred. No.: 325
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.86%
DB: 16
Length: 21
Matches: 7
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-817-318-1 (1-780) x AAR84158 (1-21)

QY 760 GTAAGCAAAAAAAAAAAAAA 780
|||||
DB 15 VALYSALALYSLSLSLS 21

RESULT 18
AAR7072
ID AAR7072 standard; peptide; 21 AA.
XX
AC AAR7072;
XX

```

XX	OS	Synthetic.	Location/Qualifiers
XX	XX	Key	1..21
XX	XX	Modified-site	/note=
XX	XX	Modified-site	"the epsilon-amino groups of the lysine residues and the alpha-amino group of the N-terminal amino acid are sufficiently methylated to impart enhanced proteolytic digestion resistance to the peptide"
XX	XX	MO9513085-A1.	
XX	XX	18-MAY-1995.	
XX	XX	01-NOV-1994;	94WO-US12550.
XX	XX	08-NOV-1993;	93US-0148889.
XX	XX	(DEME-) DEMETER BIOTECHNOLOGIES LTD.	
XX	XX	Julian GR.	
XX	XX	WPI; 1995-193900/25.	
XX	XX	New lytic peptide(s) for treating e.g. infections and neoplasias - contain mainly alanine, valine and lysine residues with the lysine residues pref. methylated	
XX	XX	Claim 8; Page 50; 66pp; English.	
XX	XX	AAR74699-R74733 are synthetic lytic peptides which are rich in the amino acids lysine, valine and alanine. They are useful in the treatment of neoplasia and viral, bacterial, protozoan, fungal or yeast infections. The lysine residues and the N-terminal amino acid residue of the peptides are methylated which imparts enhanced resistance to proteolytic digestion and allows effective in vivo administration.	
XX	XX	Sequence	21 AA;
XX	XX	Alignment Scores:	
XX	XX	Pred. No.:	325
XX	XX	Score:	7..00
XX	XX	Percent Similarity:	100.00%
XX	XX	Best local Similarity:	100.00%
XX	XX	Query Match:	2.86%
XX	XX	DB:	16
XX	XX	US-09-817-318-1 (1-780) x AAR74721 (1-21)	
XX	XX	QY 760 GTAAAGCAAAAAAAAAAAAAA 780	
XX	XX	DB 15 VallysAlaIysIysIysIys 21	
XX	XX	RESULT 20	
XX	XX	AAR64800	
XX	XX	AAR64800 standard; peptide; 21 AA.	
XX	XX	24-AUG-1995 (first entry)	
XX	XX	Amphipathic peptide #31, for treating a pulmonary disease state.	
XX	XX	Amphipathic peptide; pulmonary disease; resistant; bacteria; proteolytic digestion; methylation; glyoxylation; cystic fibrosis; CF; neoplasia; pneumonia; bronchitis; lytic activity; lysis.	
XX	XX	Synthetic.	
XX	XX	Key	Location/Qualifiers
XX	XX	Modified-site	1

FT Modified-site /note="Opt. methylated or glyoxylated"
FT 1..21 /note="Lys residues are opt. methylated"
XX
XX
PN WO9428921-A.
XX
PD 22-DEC-1994.
XX
PF 02-JUN-1994; 94WO-US06176.
XX
PR 04-JUN-1993; 93US-0039620.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
DR MPI; 1995-036106/05.
XX
PT Treatment of pulmonary disease states such as cystic fibrosis -
XX by admin. of a non-naturally occurring amphiphatic peptide
XX
PS Claim 21; Page 50; 54pp; English.
XX
CC The sequences given in AAR64770-806 and AAR76077 represent non-naturally
CC occurring amphiphatic peptides which may be used for treating
CC pulmonary disease states. These peptides have enhanced resistance
CC to proteolytic digestion due to methylation of the epsilon-amino
CC group of lys residues or glyoxylation of the side chains of Arg
CC residues, and methylation or glyoxylation of the N-terminal amino
CC acid. The peptides are prepared by standard methods of solid phase
CC synthesis and may be used in the treatment of cystic fibrosis (CF),
CC neoplasia, pneumonia, bronchitis, etc.. The peptides pref. have a
CC lytic activity, thereby lysing pathogenic bacteria, virally infected
CC cells and transformed cells as well as treating the epithelial cell
CC defect of CF.
XX
SQ Sequence 21 AA:

Alignment Scores:
Pred. No.: 325 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 16 Gaps: 0

US-09-817-318-1 (1-780) x AAR64800 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAA 780
DB 15 VallysAlaLysLysLysLys 21

RESULT 21
AAR92402
ID AAR92402 standard; peptide; 21 AA.
XX
AC AAR92402;
XX
DT 17-SEP-1996 (first entry)
XX
DE Lytic peptide used in ubiquitin-lytic peptide fusion protein.
XX
KW Ubiquitin; fusion protein; lysis; infection; neoplasia; wound healing;
KW stability; reduced toxicity.
XX
OS Synthetic.
XX
PN WO9603519-A1.
XX
PD 08-FEB-1996.
XX
PF 24-JUL-1995; 95WO-US09339.
XX

PR 22-JUL-1994; 94US-0279472.
XX
XX (DEME-) DEMETER BIOTECHNOLOGIES LTD.
PA (USDA) US SEC OF AGRIC.
XX
XX Belknap W, Garbarino J, Jaynes J;
PI MPI; 1996-117061/12.
XX
DR
XX
PT New fusion protein of ubiquitin and a lytic peptide - for treating
PT infections and neoplasia, healing wounds, etc. also related nucleic
PT acid, vectors, and transformed cells
XX
XX
PS Claim 5; Page 21; 112pp; English.
XX
CC AAR92372-R92462 are lytic peptides used to create ubiquitin-lytic
CC peptide fusion proteins in which the ubiquitin polypeptide is linked
CC at its 3'-terminus to the lytic peptide. The lytic peptides are pref.
CC selected from either the cecropins, defensins, sarcolixins, melittin
CC and magainins. The fusion proteins (FPS) are useful for treating
CC protozoal, bacterial, fungal and viral infections and neoplasia (in
CC plants and animals) in the same way as the FP alone, they also
CC promote wound healing. FPS produced in bacteria may be cleaved in
CC vitro by ubiquitin hydrolases to recover the active lytic peptide.
CC FPS produced in eukaryotic cells are cleaved by endogenous enzymes
CC to yield lytic peptide. Recombinant DNA encoding the FPS have
CC greater stability in bacteria than DNA encoding the lytic peptide
CC only.
XX
SQ Sequence 21 AA:

Alignment Scores:
Pred. No.: 325 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 17 Gaps: 0

US-09-817-318-1 (1-780) x AAR92402 (1-21)

QY 760 GTAAAGCGCAAAAAAAAAA 780
DB 15 VallysAlaLysLysLysLys 21

RESULT 22
AAR90756
ID AAR90756 standard; peptide; 21 AA.
XX
AC AAR90756;
XX
DT 17-SEP-1996 (first entry)
XX
DE Synthetic lytic peptide #86.
XX
XX Lytic peptide; ubiquitin; synthetic analogue; cell membrane; cell lysis;
KW microbial pathogen; disease-resistant plant; bacterial infection; fungus;
KW protozoa; virus; neoplasia; fusion protein; hydrolase.
XX
OS Synthetic.
XX
PN WO9603522-A1.
XX
PD 08-FEB-1996.
XX
PF 24-JUL-1995; 95WO-US09338.
XX
PR 22-JUL-1994; 94US-0279472.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes J;
XX

DR WPI: 1996-117064/12.
XX Lytic peptide(s), useful for developing disease-resistant plants -
PT can be expressed as fusion protein with ubiquitin for stable prodn.
PT In bacterial host cells
XX
PS Example 1: Page 21; 11pp; English.
XX
CC AAR89967-R90021 and AAR90726-R90763 represent synthetic analogues of
CC naturally occurring lytic peptides. Lytic peptides destroy prokaryotic
CC and other non-host cells by disrupting the cell membrane and promoting
CC cell lysis. Synthetic lytic peptide analogues have similar or higher
CC levels of lytic activity for many different types of cells, compared to
CC naturally occurring forms. The concentration of the synthetic analogue
CC required to lyse microbial pathogens does not lyse normal mammalian
CC cells. The lytic peptides can be expressed in plants to allow for the
CC development of disease-resistant plants. The peptides are useful in
CC promoting wound healing and combating bacterial infections in plants.
CC The lytic peptides can also be used for combating protozoal, fungal,
CC viral or bacterial infections or neoplasias in mammals and plants.
CC Lytic peptide-ubiquitin fusion proteins are suitable for production in
CC bacterial hosts. Bacteria lack the hydrolase which cleaves the peptide
CC from ubiquitin, and therefore the active (and cytotoxic) lytic peptide
CC will not be released in the host cells. The recombinantly produced
CC lytic peptide can be retrieved from the fusion protein by cleavage in
CC vitro.
XX
SQ Sequence 21 AA:

Alignment Scores:
Pred. No.: 325 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x AAR90756 (1-21)
OY 760 GTAAAGCGCAAAAAAAAAA 780
|||||
Db 15 VallySAAlaLysLysLysLys 21

RESULT 23
AAM39773
ID AAM39773 standard; peptide: 21 AA.
XX
AC AAM39773:
XX
DT 20-MAY-1998 (first entry)
XX
DE Synthetic lysine-rich lytic peptide 24.
XX
KW Lytic peptide; lysine-rich; proteolytic digestion; methylation; trypsin;
KW protection; amphipathic alpha-helix; beta-pleated sheet; treatment;
KW infection; viral; bacterial; yeast; fungal; protozoan; cancer.
XX
OS Synthetic.
XX
PN US5717064-A.
XX
PD 10-FEB-1998.
XX
PF 24-APR-1995: 95US-0427001.
XX
PR 24-APR-1995: 95US-0427001.
PR 18-NOV-1993: 93US-0148889.
XX
PA (DEME-) DEMETER BIOTECHNOLOGIES LTD.
XX
PI Jaynes JM, Julian GR;
XX
WPI: 1998-158370/14.

XX
PT Cytolytic peptide analogues - with methylated lysine residues to
PT increase protease resistance
XX
XX Claim 1; Column 25-26; 21pp; English.
PS
CC Peptides AAM39750-W39785 represent a family of synthetic lytic peptides
CC which are stabilised by having methylated epsilon-amino groups at
CC their lysine residues. Peptides AAM39750-W39771 and AAM39781-W39785 have
CC an amphipathic alpha-helix conformation while peptides AAM39772-W39780
CC have a beta-pleated sheet conformation. These peptides have enhanced
CC resistance to proteolytic digestion by trypsin. Such peptides can be used
CC to treat infections by lysing bacterial, yeast, fungal and protozoan
CC cells or to treat cancers by lysing neoplastic or transformed cells. They
CC can also be used to treat viral infections by lysing enveloped viruses
CC and virus-infected cells.
XX
SQ Sequence 21 AA:

Alignment Scores:
Pred. No.: 325 Length: 21
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x AAM39773 (1-21)
OY 760 GTAAAGCGCAAAAAAAAAA 780
|||||
Db 15 VallySAAlaLysLysLysLys 21

RESULT 24
ABG27285
ID ABG27285 standard; Protein; 28 AA.
XX
AC ABG27285:
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27276.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS91472.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID No 57644; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations in
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pcl_sequences.

SO Sequence 28 AA;

Alignment Scores:

Pred. No.:	319	Length:	28
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	22	Gaps:	0

US-09-817-318-1 (1-780) x ABG27285 (1-28)

OY 339 TCACGTGCAAAATTCATGAA 319

Db 16 SerLeuSerLysIleHisGlu 22

RESULT 25

AAV68253

ID AAV68253 standard; Peptide: 38 AA.

AC AAV68253;

DT 13-APR-2000 (first entry)

DE Murine class I molecule related protein sequence SEQ ID NO:85.

KW MHC class I; major histocompatibility complex; microglobulin; antigen;

KW immune response; immunisation; AIDS; multiple sclerosis; toxic shock;

KW cancer; lupus erythematosus; snake bite; cytostatic; antiviral;

KW immunomodulatory; dermatological; immunosuppressive; antiinflammatory;

XX neoprotective.

OS Mus sp.

XX US6011146-A.

PN 04-JAN-2000.

PD 07-JUN-1995;

PF 95US-0481985.

PR 15-NOV-1991;

PR 05-DEC-1991;

XX 91US-0801818.

XX (INSP) INST PASTEUR.

PA (INRM) INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Mottez E, Abastado J;

XX WPI; 2000-125951/11.

XX Disclosure: Column 99-100; 88pp; English.
PS
XX The present invention describes a recombinant DNA molecule (I)
CC containing a sequence (Ia) that encodes an altered MHC (major
CC histocompatibility complex) Class I determinant (II) comprises a
CC polypeptide with alpha1, alpha2, alpha3 and beta2-microglobulin
CC domains, in which alpha3 and beta2 are covalently linked, thorough C-
CC and N-termini respectively, via a nucleotide spacer sequence encoding a
CC polypeptide. (II) includes an antigen-binding site and when (II) and
CC the antigen are associated they are recognized by a mammalian T cell
CC receptor (TCR). (I) are used to produce (II) which are used to study
CC functional interactions between the various MHC domains. They can also
CC be used to modulate (in vivo or in vitro) the immune system by inducing
CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)
CC of immune system cells, typically for treating, or immunising against;
CC cancer, acquired immune deficiency syndrome, lupus erythematosus,
CC multiple sclerosis, toxic shock and snake bite, but also for selective
CC destruction of autoreactive cells, diagnostically to assay T cell
CC receptors and to raise specific antibodies (useful for diagnosis,
CC therapy, studying MHC-associated cellular processes and for affinity
CC purification). AAV57558 and AAV68186 to AAV68316 are sequences used in
CC the exemplification of the present invention.

SO Sequence 38 AA;

Alignment Scores:

Pred. No.:	313	Length:	38
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	21	Gaps:	0

US-09-817-318-1 (1-780) x AAV68253 (1-38)

OY 625 ACTTGTGATTATCCGCGCC 605

Db 19 ThrSerAspSerLeuPro 25

RESULT 26

AAV52907

ID AAV52907 standard; Peptide: 38 AA.

AC AAV52907;

DT 14-FEB-2000 (first entry)

DE Murine class I molecule H-2K-d peptide SEQ ID NO:85.

KW Major histocompatibility complex; MHC class I; MHC class II; antigen;

KW immune response; diagnosis; antibody; immunisation; autoimmune disease;

KW acquired immune deficiency syndrome; AIDS; cytostatic; dermatological;

KW anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;

KW vaccine; lupus erythematosus; multiple sclerosis; thyroiditis;

KW toxic shock; tumour; snakebite.

XX Mus sp.

XX US5976551-A.

PN 02-NOV-1999.

PD 07-JUN-1995;

PF 95US-0484905.

PR 05-DEC-1991;

PR 15-NOV-1991;

XX 91US-0801818.

XX (INSP) INST PASTEUR.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

PI Kourilsky P, Mottez E, Abastado J;

XX New recombinant DNA encoding covalently linked form of major

PT histocompatibility complex Class I determinant, used for immune system

PI stimulation, e.g. for treating cancer

XX

DR WPI: 2000-037081/03.
XX
XX Composition containing an antigen and altered major histocompatibility
PT Class II determinant, used to immunize against autoimmune diseases,
PT e.g. acquired immune deficiency syndrome -
XX
XX
PS Disclosure: Column 123-124; 96pp; English.
XX
XX The present invention describes a composition capable of eliciting
CC anti-major histocompatibility (MHC) antibodies. The composition
CC comprises an antigen associated with an altered MHC Class II determinant
CC (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains
CC encoded by a mammalian MHC Class II locus covalently linked to form a
CC polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in
CC sequence. The resulting Antigen-MHC complex is recognizable by the T cell
CC receptor. The compositions are used for immunisation against, or
CC treatment of, a wide range of autoimmune diseases, e.g. acquired immune
CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,
CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature
CC of antigen. (I) is also used to analyse functional interactions between
CC the various domains and for targeting lymphocyte receptors. Antibodies
CC against (I) are produced by usual methods of immunisation or cell fusion,
CC and may be humanised by standard methods. These antibodies are useful for
CC diagnosis (detection or purification of MHC gene products), therapy
CC (neutralising MHC on cell surfaces) and in the study of MHC and cellular
CC processes. AA233240 to AA233242 and AA52840 to AA52970 represent
CC sequences used in the exemplification of the present invention.
XX
XX S0 Sequence 38 AA:
XX
XX Alignment Scores:
Pred. No.: 313 Length: 38
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 21 Gaps: 0
US-09-817-318-1 (1-780) x AA52907 (1-38)
OY 625 ACTTCTGATTATCCCTGCC 605
XXXXXXXXXXXXXXXXXXXX
DB 19 ThrSerAspLeuSerLeuPro 25
RESULT 27
AAB58668
ID AAB58668 standard; protein; 38 AA.
XX
XX AAB58668;
XX
XX 13-MAR-2001 (first entry)
XX
XX Murine class I protein #5.
XX
XX Major histocompatibility complex: MHC class I; immune; snake bite;
KM T cell mediated autoimmune disease; AIDS; lupus erythematosus;
KM toxic shock.
XX
XX Mus musculus.
OS
XX
XX US6153408-A.
PN
XX
XX 28-NOV-2000.
PD
XX
XX 09-JAN-1995; 95US-0370476.
XX
XX 15-NOV-1991; 91US-0792473.
PR 07-SEP-1993; 93US-0117575.
PR 05-DEC-1991; 91US-0801818.
PR 07-JUN-1993; 93US-0072787.
XX
XX (INSP) INST PASTEUR.
PA (INRM) INST NAT SANTE & RECH MEDICAL.
XX

XX
XX Abastado J, Kourilsky P, Castrouge A, Ojcius D, Lone Y, Mottez E;
PI WPI: 2001-060089/07.
XX
XX
XX
XX New altered major histocompatibility complex (MHC) class I determinant
PT useful for eliciting an immune response and/or for immunizing against
PT or treating diseases, for example, multiple sclerosis, AIDS, toxic
PT shock or snake bite -
XX
XX
PS Disclosure: Column 19-26; 105pp; English.
XX
XX The present invention relates to a major histocompatibility complex
CC (MHC) class I determinant, which has alpha_1 alpha_2 alpha_3 and
CC beta2-microglobulin polypeptide domains encoded by a mammalian MHC
CC class I locus. The MHC class I determinants are useful for activating
CC the immune system and presenting antigens to the immune system to
CC elicit an antigenic response. The MHC class I determinants are also
CC useful for treating diseases, e.g. T cell mediated autoimmune disease,
CC AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC
CC class I determinants and compositions containing antigens bound to
CC the determinants are useful in diagnostic applications, e.g. altered
CC determinants may be used to target lymphocyte receptors and the
CC resulting bound determinant can be assayed.
XX
XX S0 Sequence 38 AA:
XX
XX Alignment Scores:
Pred. No.: 313 Length: 38
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 22 Gaps: 0
US-09-817-318-1 (1-780) x AAB58668 (1-38)
OY 625 ACTTCTGATTATCCCTGCC 605
XXXXXXXXXXXXXXXXXXXX
DB 19 ThrSerAspLeuSerLeuPro 25
RESULT 28
AA568254
ID AA568254 standard; peptide; 42 AA.
XX
XX AA568254;
XX
XX 13-APR-2000 (first entry)
XX
XX Murine class I molecule related protein sequence SEQ ID NO:86.
XX
XX MHC class I; major histocompatibility complex; microglobulin; antigen;
XX immune response; immunisation; AIDS; multiple sclerosis; toxic shock;
KM cancer; lupus erythematosus; snake bite; cytostatic; antiviral;
KM immunomodulatory; dermatological; immunosuppressive; antiinflammatory;
KM neuroprotective.
XX
XX Mus sp.
OS
XX
XX US6011146-A.
PN
XX
XX 04-JAN-2000.
PD
XX
XX 07-JUN-1995; 95US-0481985.
XX
XX 15-NOV-1991; 91US-0792473.
PR 05-DEC-1991; 91US-0801818.
XX
XX (INSP) INST PASTEUR.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
XX Kourilsky P, Mottez E, Abastado J;
PI

DR WPI: 2000-125951/11.
 XX New recombinant DNA encoding covalently linked form of major
 PT histocompatibility complex Class I determinant, used for immune system
 PT stimulation, e.g. for treating cancer -
 XX
 XX
 PS Disclosure: Column 99-100; 88pp; English.
 CC The present invention describes a recombinant DNA molecule (I)
 CC containing a sequence (Ia) that encodes an altered MHC (major
 CC histocompatibility complex) Class I determinant (II) comprises a
 CC polypeptide with alpha1, alpha2, alpha3 and beta2 microglobulin
 CC domains, in which alpha1 and beta2 are covalently linked, thorough C-
 CC and N-termini respectively, via a nucleotide spacer sequence encoding a
 CC polypeptide. (II) includes an antigen-binding site and when (II) and
 CC the antigen are associated they are recognized by a mammalian T cell
 CC receptor (TCR). (I) are used to produce (II) which are used to study
 CC functional interactions between the various MHC domains. They can also
 CC be used to modulate (in vivo or in vitro) the immune system by inducing
 CC an effector response (cytotoxicity, antibody synthesis, phagocytosis)
 CC of immune system cells, typically for treating, or immunising against;
 CC cancer, acquired immune deficiency syndrome, lupus erythematosus,
 CC multiple sclerosis, toxic shock and snake bite, but also for selective
 CC destruction of autoreactive cells, diagnostically to assay T cell
 CC receptors and to raise specific antibodies (useful for diagnosis,
 CC therapy, studying MHC-associated cellular processes and for affinity
 CC purification). AA57558 and AA568186 to AA568316 are sequences used in
 CC the exemplification of the present invention.
 XX
 SO Sequence 42 AA:
 Alignment Scores:
 Pred. No.: 310 Length: 42
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 21 Gaps: 0
 US-09-817-318-1 (1-780) x AA568254 (1-42)
 OY 625 ACTTCTGATTATCCCTGCC 605
 DB 23 ThrSerAspLeuSerLeupro 29
 RESULT 29
 AA52908
 ID AA52908 standard; Peptide: 42 AA.
 XX
 AC AA52908;
 XX
 DT 14-FEB-2000 (first entry)
 XX
 DE Murine class I molecule H-2K-q peptide SEQ ID NO:86.
 XX
 XX Major histocompatibility complex; MHC class I; MHC class II; antigen;
 KW immune response; diagnosis; antibody; immunisation; autoimmune disease;
 KW acquired immune deficiency syndrome; AIDS; cytostatic; dermatological;
 KW anti-inflammatory; neuroprotective; immunosuppressive; antithyroid;
 KW vaccine; lupus erythematosus; multiple sclerosis; thyroiditis;
 KW toxic shock; tumour; snakebite.
 XX
 OS Mus sp.
 XX
 PN US5976551-A.
 XX
 PD 02-NOV-1999.
 XX
 PF 07-JUN-1995; 95US-0484905.
 XX
 PR 05-DEC-1991; 91US-0801818.
 PR 15-NOV-1991; 91US-0792473.
 XX

PA (INSP) INST PASTEUR.
 PA (INNM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Kourilsky P, Mottez E, Abastado J;
 XX
 DR WPI: 2000-037081/03.
 XX
 PT Composition containing an antigen and altered major histocompatibility
 PT Class II determinant, used to immunize against autoimmune diseases,
 PT e.g. acquired immune deficiency syndrome -
 XX
 PS Disclosure: Column 123-124; 96pp; English.
 XX
 CC The present invention describes a composition capable of eliciting
 CC anti-major histocompatibility (MHC) antibodies. The composition
 CC comprises an antigen associated with an altered MHC Class II determinant
 CC (I) comprising alpha1, alpha2, beta1 and beta2 polypeptide domains
 CC encoded by a mammalian MHC Class II locus covalently linked to form a
 CC polypeptide (I) containing beta2, alpha2, alpha1 and beta1 domains in
 CC sequence. The resulting Antigen-MHC complex is recognizable by the T cell
 CC receptor. The compositions are used for immunisation against, or
 CC treatment of, a wide range of autoimmune diseases, e.g. acquired immune
 CC deficiency syndrome (AIDS), lupus erythematosus, multiple sclerosis,
 CC thyroiditis, toxic shock, tumour and snakebite, depending on the nature
 CC of antigen. (I) is also used to analyse functional interactions between
 CC the various domains and for targeting lymphocyte receptors. Antibodies
 CC against (I) are produced by usual methods of immunisation or cell fusion,
 CC and may be humanised by standard methods. These antibodies are useful for
 CC diagnosis (detection or purification of MHC gene products), therapy
 CC (neutralising MHC on cell surfaces) and in the study of MHC and cellular
 CC processes. AA33240 to AA33242 and AA52840 to AA52970 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SO Sequence 42 AA:
 Alignment Scores:
 Pred. No.: 310 Length: 42
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 21 Gaps: 0
 US-09-817-318-1 (1-780) x AA52908 (1-42)
 OY 625 ACTTCTGATTATCCCTGCC 605
 DB 23 ThrSerAspLeuSerLeupro 29
 RESULT 30
 AAM87287
 ID AAM87287 standard; Protein: 42 AA.
 XX
 AC AAM87287;
 XX
 DT 07-NOV-2001 (first entry)
 XX
 DE Human immune/haematopoietic antigen SEQ ID NO:14880.
 XX
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 KW
 OS Homo sapiens.
 XX
 PN WO200157182-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01354.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 24-FEB-2000; 2000US-0184664.
 XX

PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230457.
PR 06-SEP-2000; 2000US-0230458.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.

PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249254.
PR 17-NOV-2000; 2000US-0249255.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 03-DEC-2000; 2000US-0251030.
PR 03-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251989.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI
PI
XX
XX
DR
DR
DR
XX
XX
PT
PT
XX
XX
PS
Claim 11: SEO ID NO 14880; 3071pp + Sequence Listing: English.

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX

SQ Sequence 42 AA;

Alignment Scores:

Pred. No.:	310	Length:	42
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	22	Gaps:	0

US-09-817-318-1 (1-780) x AAM87287 (1-42)

OY 238 TTACAGACCTTACTCTTCAC 258

Db 10 PherthrapsleuThrLeuHis 16

RESULT 31

AA58669 standard; protein; 42 AA.

XX AAB58669;

DT 13-MAR-2001 (first entry)

DE Murine class I protein #6.

XX Major histocompatibility complex; MHC class I; immune; snake bite;

KW T cell mediated autoimmune disease; AIDS; lupus erythematosus;

XX toxic shock.

OS Mus musculus.

PN US6153408-A.

PD 28-NOV-2000.

PF 09-JAN-1995; 95US-0370476.

PR 15-NOV-1991; 91US-0792473.

PR 07-SEP-1993; 93US-0117575.

PR 05-DEC-1991; 91US-0801818.

PR 07-JUN-1993; 93US-0072787.

PA (INSP) INST PASTEUR.

PA (INRM) INST NAT SANTE & RECH MEDICAL.

PI Abastado J, Kourilsky P, Castrouge A, Ojcius D, Lone Y, Mottez E;

DR WPI; 2001-06089/07.

XX New altered major histocompatibility complex (MHC) class I determinant

PT useful for eliciting an immune response and/or for immunizing against

PT or treating diseases, for example, multiple sclerosis, AIDS, toxic

PT shock or snake bite

XX Disclosure; Column 19-26; 105pp; English.

XX The present invention relates to a major histocompatibility complex
XX (MHC) class I determinant, which has alpha_1 alpha_2 alpha_3 and
XX beta2-microglobulin polypeptide domains encoded by a mammalian MHC
XX class I locus. The MHC class I determinants are useful for activating
XX the immune system and presenting antigens to the immune system to
XX elicit an antigenic response. The MHC class I determinants are also
XX useful for treating diseases, e.g. T cell mediated autoimmune disease,
XX AIDS, lupus erythematosus, toxic shock or snake bite. The altered MHC
XX class I determinants and compositions containing antigens bound to
XX the determinants are useful in diagnostic applications, e.g. altered
XX determinants may be used to target lymphocyte receptors and the
XX resulting bound determinant can be assayed.

SQ Sequence 42 AA;

Alignment Scores:

Pred. No.:	310	Length:	42
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	22	Gaps:	0

US-09-817-318-1 (1-780) x AAB58669 (1-42)

OY 625 ACTTCGATTATCCCTGCC 605

Db 23 ThrSerAspleuSerLeuPro 29

RESULT 32

ABG01742 standard; protein; 46 AA.

XX ABG01742;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #1733.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PA Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS65929.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX diagnostics, forensics, gene mapping, identification of mutations

XX responsible for genetic disorders or other traits and to assess

XX biodiversity

XX Claim 20; SEQ ID No 32101; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

XX polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantifying a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABO00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 46 AA:

Alignment Scores:

Pred. No.:	309	Length:	46
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	22	Gaps:	0

US-09-817-318-1 (1-780) x ABO01742 (1-46)

OY 701 GTTTAATTCTCCGGTTGA 721

Db 17 ValLeuIleLeuValVal 23

RESULT 33

AAB63839

ID AAB63839 standard; Protein: 71 AA.

XX AAB63839.

XX AC

XX DT

26-MAR-2001 (first entry)

XX DE

Human prostate cancer associated antigen protein sequence SEQ ID NO:1201.

XX KM

Human: breast cancer; gastric cancer; prostate cancer; diagnosis;

XX KW

cancer associated antigen; cytosolic; cancer vaccine.

XX OS

Homo sapiens.

XX PN

WO200073801-A2.

XX PD

07-DEC-2000.

XX PF

26-MAY-2000; 2000WO-US14749.

XX PR

28-MAY-1999; 99US-0136526.

XX PT

10-SEP-1999; 99US-0153454.

XX PA

(LUDW-) LUDWIG INST CANCER RES.

XX PI

Obata Y;

XX DR

WPI; 2001-025274/03.

XX PT

Nucleic acids encoding breast, gastric and prostate cancer associated

XX PT

antigen precursors, useful for diagnosing and treating a condition

XX PT

characterized by expression of an abnormal amount of a protein, e.g.

XX cancer -

Example 1; Page 741; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014

CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB62232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytosolic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.

XX SQ Sequence 71 AA:

Alignment Scores:

Pred. No.:	300	Length:	71
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	22	Gaps:	0

US-09-817-318-1 (1-780) x AAB63839 (1-71)

OY 649 AACATACTTGTATTGACA 629

Db 2 AsnIleIhrLeuLeuThr 8

RESULT 34

AAB63843

ID AAB63843 standard; Protein: 71 AA.

XX AAB63843.

XX AC

26-MAR-2001 (first entry)

XX DT

Human prostate cancer associated antigen protein sequence SEQ ID NO:1205.

XX DE

Human: breast cancer; gastric cancer; prostate cancer; diagnosis;

XX KW

cancer associated antigen; cytosolic; cancer vaccine.

XX OS

Homo sapiens.

XX PN

WO200073801-A2.

XX PD

07-DEC-2000.

XX PF

26-MAY-2000; 2000WO-US14749.

XX PR

28-MAY-1999; 99US-0136526.

XX PT

10-SEP-1999; 99US-0153454.

XX PA

(LUDW-) LUDWIG INST CANCER RES.

XX PI

Obata Y;

XX DR

WPI; 2001-025274/03.

XX PT

Nucleic acids encoding breast, gastric and prostate cancer associated

XX PT

antigen precursors, useful for diagnosing and treating a condition

XX PT

characterized by expression of an abnormal amount of a protein, e.g.

XX cancer -

Example 1; Page 742; 799pp; English.

XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014

XX CC

represent nucleotide sequences encoding human breast, gastric and

XX CC

prostate cancer associated antigen precursors (CAAP) respectively.

XX CC

AAB62232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970

XX Sequence 71 AA:
 Alignment Scores:
 Pred. No.: 300 Length: 71
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 22 Gaps: 0

US-09-817-318-1 (1-780) x AAB63843 (1-71)
 QY 649 AACATACCTTGTATTGACA 629
 DB 2 Asn11erHrleuLeuThr 8

RESULT 35
 AAM07875
 ID AAM07875 standard; Protein: 87 AA.
 XX
 AC AAM07875;
 XX
 DT 22-JUL-1997 (first entry)
 XX
 DE Protein reactive with multiple sclerosis antibodies.
 XX
 KW Mitochondrion; electron; transport; chain; ND4; antigen; protein;
 KM multiple sclerosis; antibody; immunoassay; detection; damage;
 KW spirochaete; surface; preparation; anti-idiotypic; treatment.
 XX
 OS Homo sapiens.
 XX
 PN WO9630398-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 25-MAR-1996; 96WO-AU00166.
 XX
 PR 18-DEC-1995; 95AU-0007205.
 PR 24-MAR-1995; 95AU-0001974.
 XX
 PA (UYMU-) UNITV MURDOCH.
 XX
 PI Carnegie PR, Sanati MH;
 XX
 DR WPI: 1996-505781/50.
 DR N-PSDB: AAT44603.
 XX
 PT DNA encoding a polypeptide reactive with multiple sclerosis-induced
 PT antibodies - used in an immunoassay to detect mitochondrial damage,
 PT and to prepare anti-idiotypic antibodies for therapy.
 XX
 PS Claim 2; Page 39; 61pp; English.
 XX
 CC The present sequence, which is encoded by a nucleotide sequence
 CC having greater than 98% identity with a portion of the
 CC mitochondrial gene encoding the mitochondrial electron transport
 CC chain protein ND4, is a polypeptide immunologically reactive with
 CC multiple sclerosis (MS) induced antibodies (Ab). The polypeptide
 CC can be used in an immunoassay to detect mitochondrial damage, and
 CC Ab reactive with spirochaete surface and mitochondrial proteins.
 CC It can also be used to prepare anti-idiotypic Ab for MS treatment.
 XX
 SO Sequence 87 AA:

Alignment Scores:
 Pred. No.: 295 Length: 87
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 17 Gaps: 0

US-09-817-318-1 (1-780) x AAM07875 (1-87)
 QY 649 AACATACCTTGTATTGACA 629
 DB 77 Asn11erHrleuLeuThr 83

RESULT 36
 AAG03475
 ID AAG03475 standard; Protein: 87 AA.
 XX
 AC AAG03475;
 XX
 DT 06-OCT-2000 (first entry)
 XX
 DE Human secreted protein, SEQ ID NO: 7556.
 XX
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-0200610.
 XX
 PR 26-FEB-1999; 99US-0122487.
 XX
 PA (GEST) GENSET.
 XX
 PI Dunas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI: 2000-500381/45.
 DR N-PSDB: AAC03481.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 PS Claim 13; SEQ ID 7556; 71pp + CD-ROM; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SO Sequence 87 AA:

Alignment Scores:
 Pred. No.: 295 Length: 87
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 21 Gaps: 0

US-09-817-318-1 (1-780) x AAG03475 (1-87)
 QY 673 TTATCACCCTATAATACCA 653
 DB 23 LeuSerProLeuLysTyrPro 29

```
RESULT 37
AA12861
ID AAY12861 standard; Protein: 88 AA.
XX
AC AAY12861;
XX
DT 21-JUN-1999 (first entry)
XX
DE Human 5' EST secreted protein SEQ ID NO:451.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition.
XX
OS Homo sapiens.
XX
PN MO9906549-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98MO-IB01231.
XX
PR 01-AUG-1997; 97US-0905279.
XX
PA (GEST ) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI: 1999-153779/13.
XX
DR N-PSDB: AAX51639.
XX
PT New nucleic acids encoding human secreted proteins - obtained from
PT cDNA libraries derived from testis, ovary, uterus and spleen tissue
XX
PS Claim 34; Page 489-490; 522pp; English.
XX
CC AAY51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12681 to
CC AAY12913, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell.
XX
SQ Sequence 88 AA:
XX
Alignment Scores:
Pred. No.: 295 Length: 88
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 20 Gaps: 0
US-09-817-318-1 (1-780) x AAY12861 (1-88)
OY 673 TTATACCTATTAATACCA 653
DB 23 LeuSerProIleIysTyrPro 29
```

```
RESULT 38
AA07086
ID AA07086 standard; Protein: 88 AA.
XX
AC AA07086;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 20978.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX
PR 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
XX
DR N-PSDB: AA187017.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 20978; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 88 AA:
XX
Alignment Scores:
Pred. No.: 295 Length: 88
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 22 Gaps: 0
US-09-817-318-1 (1-780) x AA07086 (1-88)
OY 248 TTACTCTGACATTTGACTTG 268
DB 78 LeuLeuPheThrIleAspIleu 84
RESULT 39
ABP03162
ID ABP03162 standard; Protein: 91 AA.
```

XX	ABP03162:	
AC		
XX		
DT	24-JUN-2002 (first entry)	
XX		
DE	Human ORFX protein sequence SEQ ID NO:6306.	
XX		
KW	Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;	
KW	hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;	
KW	degenerative disorder; osteoarthritis; neurodegenerative disorder;	
KW	cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;	
KW	hypertension; hypothyroidism; cholesterol ester storage disease;	
KW	immune deficiency; immune disorder; infectious disease;	
KW	autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;	
KW	myasthenia gravis.	
OS	Homo sapiens.	
PN	WO20019523-A2.	
XX		
PD	06-DEC-2001.	
XX		
PF	29-MAY-2001: 2001WO-US10836.	
XX		
PR	30-MAY-2000: 2000US-206132P.	
PR	29-AUG-2000: 2000US-228716P.	
PA	(CUBA-) CUBAGEN CORP.	
PI	Shinkets RA, Leach MD;	
DR	MPI: 2002-106308/14.	
DR	N-PSTDB: ABN18914.	
PT	Novel human polypeptides and polynucleotides useful for diagnosing,	
PT	preventing and treating cardiovascular disease, neurodegenerative,	
PT	hyperproliferative disorders and autoimmune disorders	
PS	Disclosure: SEQ ID 6306; 1037bp; English.	
XX		
CC	The present invention describes substantially purified human proteins	
CC	(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1	
CC	in the specification). ABN15762 to ABN27252 encode the human ORFX	
CC	proteins given in ABP00010 to ABP11500. ORFX proteins are useful for	
CC	treating or preventing a pathology associated with an ORFX-associated	
CC	disorder in humans, and in the manufacture of a medicament for treating a	
CC	syndrome associated with ORFX-associated disorder. ORFX polynucleotide	
CC	sequences can be used in gene therapy. ORFX sequences can be used in the	
CC	treatment of cancer, hyperproliferative disorders, cirrhosis of liver,	
CC	psoriasis, benign tumours, keloid, degenerative disorders, hemorrhage,	
CC	osteoarthritis, neurodegenerative disorders, disorders related to organ	
CC	transplantation, cardiovascular diseases, diabetes mellitus, systemic	
CC	lupus erythematosus, hypertension, hypothyroidism, cholesterol ester	
CC	storage disease, various immune deficiencies and disorders, infectious	
CC	diseases, autoimmune disorders such as multiple sclerosis, rheumatoid	
CC	arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host	
CC	disease and autoimmune inflammatory eye disease. ORFX proteins are also	
CC	useful for treating burns, incisions, ulcers, for treating osteoporosis,	
CC	bone degenerative disorders, or periodontal disease, and for gut	
CC	protection or regeneration and treatment of lung or liver fibrosis,	
CC	reperfusion injury in various tissues and conditions resulting from	
CC	systemic cytokine damage.	
CC	N.B. The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences.	
XX		
SO	Sequence 91 AA:	
<hr/>		
Alignment Scores:		
Pred. NO.:	295	Length: 91
Score:	7.00	Matches: 7
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0

Query Match:	2,928	Indels:	0
DB:	23	Gaps:	0
US-09-817-318-1 (1-780) x ABP03162 (1-91)			
OY 736 CCAGAGTCACGATATTACAC 716			
Db 16 ProGluSerProIrryTrasn 22			
RESULT 40			
AAG25318			
ID AAG25318 standard; Protein: 94 AA.			
XX AAG25318;			
XX AC			
XX DT 17-OCT-2000 (first entry)			
XX DE Zea mays protein fragment SEO ID NO: 29332.			
XX KW Protein identification; signal transduction pathway; metabolic pathway;			
XX KW hybridisation assay; genetic mapping; gene expression control; promoter,			
XX KW termination sequence; corn.			
XX OS Zea mays subsp. mays.			
XX PN EP1033405-A2.			
XX PD 06-SEP-2000.			
XX PF 25-FEB-2000; 2000EP-0301439.			
XX PR 25-FEB-1999; 99US-0121825.			
XX PR 05-MAR-1999; 99US-0123180.			
XX PR 09-MAR-1999; 99US-0123548.			
XX PR 23-MAR-1999; 99US-0125788.			
XX PR 25-MAR-1999; 99US-0126264.			
XX PR 29-MAR-1999; 99US-0126785.			
XX PR 01-APR-1999; 99US-0127462.			
XX PR 06-APR-1999; 99US-0128234.			
XX PR 08-APR-1999; 99US-0128714.			
XX PR 16-APR-1999; 99US-0129845.			
XX PR 19-APR-1999; 99US-0130077.			
XX PR 21-APR-1999; 99US-0130449.			
XX PR 23-APR-1999; 99US-0130510.			
XX PR 28-APR-1999; 99US-0130891.			
XX PR 30-APR-1999; 99US-0131449.			
XX PR 30-APR-1999; 99US-0132048.			
XX PR 04-MAY-1999; 99US-0132407.			
XX PR 05-MAY-1999; 99US-0132484.			
XX PR 06-MAY-1999; 99US-0132485.			
XX PR 07-MAY-1999; 99US-0132486.			
XX PR 11-MAY-1999; 99US-0132487.			
XX PR 14-MAY-1999; 99US-0132863.			
XX PR 14-MAY-1999; 99US-0134218.			
XX PR 14-MAY-1999; 99US-0134219.			
XX PR 18-MAY-1999; 99US-0134370.			
XX PR 19-MAY-1999; 99US-0134768.			
XX PR 20-MAY-1999; 99US-0134941.			
XX PR 21-MAY-1999; 99US-0135124.			
XX PR 24-MAY-1999; 99US-0135353.			
XX PR 25-MAY-1999; 99US-0135629.			
XX PR 27-MAY-1999; 99US-0136021.			
XX PR 28-MAY-1999; 99US-0136392.			
XX PR 01-JUN-1999; 99US-0136782.			
XX PR 03-JUN-1999; 99US-0137222.			
XX PR 04-JUN-1999; 99US-0137528.			
XX PR 07-JUN-1999; 99US-0137502.			
XX PR 08-JUN-1999; 99US-0137724.			
XX PR 10-JUN-1999; 99US-0138094.			
XX PR 10-JUN-1999; 99US-0138540.			
XX PR 10-JUN-1999; 99US-0138847.			

PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139452.
PR 17-JUN-1999; 9905-0139453.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141842.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.
PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144684.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
PR 23-JUL-1999; 9905-0145218.
PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 03-AUG-1999; 9905-0146389.
PR 04-AUG-1999; 9905-0147038.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 06-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 09-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.

PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.
PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149175.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154039.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.
PR 23-SEP-1999; 9905-0155486.
PR 24-SEP-1999; 9905-0155659.
PR 28-SEP-1999; 9905-0156458.
PR 29-SEP-1999; 9905-0156599.
PR 04-OCT-1999; 9905-0157117.
PR 05-OCT-1999; 9905-0157753.
PR 06-OCT-1999; 9905-0157865.
PR 07-OCT-1999; 9905-0158029.
PR 08-OCT-1999; 9905-0158232.
PR 12-OCT-1999; 9905-0158369.
PR 13-OCT-1999; 9905-0159293.
PR 13-OCT-1999; 9905-0159294.
PR 13-OCT-1999; 9905-0159295.
PR 14-OCT-1999; 9905-0159320.
PR 14-OCT-1999; 9905-0159339.
PR 14-OCT-1999; 9905-0159337.
PR 14-OCT-1999; 9905-0159637.
PR 14-OCT-1999; 9905-0159638.
PR 18-OCT-1999; 9905-0159584.
PR 21-OCT-1999; 9905-0160741.
PR 21-OCT-1999; 9905-0160767.
PR 21-OCT-1999; 9905-0160770.
PR 21-OCT-1999; 9905-0160814.
PR 21-OCT-1999; 9905-0160815.
PR 22-OCT-1999; 9905-0160980.
PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
PR 25-OCT-1999; 9905-0161404.
PR 25-OCT-1999; 9905-0161405.
PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.
PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Alignment Scores:

Pred. No.:	294	Length:	94
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	21	Gaps:	0

US-09-817-318-1 (1-780) x AAG25318 (1-94)

QY 418 TCTTCTGTGAGTTCCTTGCC 438
 |||
 Db 79 SerSerValSerSerPheAla 85

RESULT 41

ABB80897
 ID ABB80897 standard; Protein: 97 AA.

AC ABB80897;

XX 08-OCT-2002 (first entry)

XX Murine eotaxin polypeptide.

XX Eotaxin: eosinophil; chemotaxis; cytostatic; antiinflammatory; cardiant;
 KW antiallergic; immunosuppressive; antiasthmatic; antiparasitic; histamine;
 KW dermatological; vasotropic; gene therapy; antianaphylactic; mouse.

XX Mus musculus.

FH Key Location/Qualifiers

FT Peptide 1..23

FT /note- "signal peptide"

FT Protein 24..97

XX /note- "mature protein"

PN US6403782-B1.

PD 11-JUN-2002.

XX 04-AUG-1999; 99US-0366887.

XX 22-JUN-1995; 95US-000449P.

PR 01-SEP-1995; 95US-0522713.

XX (HARD) HARVARD COLLEGE.

PA (GEHO) GEN HOSPITAL CORP.

XX Luster AD, Leder P, Rothenberg M, Garcia E;

DR WPI; 2002-565447/60.

DR N-PSDB; ABBN6331.

XX New DNA encoding murine, guinea pig or human eotaxin polypeptides.

PT useful for treating inflammation and tumorigenesis and in anticancer

PT gene therapy -

XX Claim 1; Fig 3A; 42pp; English.

XX The invention relates to polynucleotides encoding murine, guinea pig or
 CC human eotaxin polypeptides. The eotaxin polynucleotides are useful for
 CC modulating eosinophil chemotaxis, for increasing eosinophil chemotactic
 CC events, and for improving prognosis with tumours in patients. They are
 CC also useful for treating inflammation and tumourigenesis, and for
 CC reducing inflammation and cytotoxic damage caused by eosinophils, for
 CC e.g. during asthmatic reactions, eosinophilic pneumonia and allergic
 CC diseases, inflammatory bowel diseases, atopic dermatitis, urticaria,
 CC vasculitis, parasitic infections and eosinophil cardiac diseases. The
 CC eotaxin polynucleotides are also useful for modulating histamine release
 CC by modulating eotaxin activity or expression during anaphylaxis,
 CC urticaria and allergic reactions. They are useful for detecting and
 CC monitoring eosinophil mediating conditions, and in anti-cancer gene
 CC therapy. The present sequence represents the murine eotaxin.

XX Sequence 97 AA;

Alignment Scores:

Pred. No.: 293

Score: 7.00

Percent Similarity: 100.00%

Length: 97

Matches: 7

Conservative: 0

Best Local Similarity: 100.00%
 Query Match: 2.92%
 DB: 23
 Gaps: 0

US-09-817-318-1 (1-780) x ABB80897 (1-97)

QY 640 TTGTTATTGACAGTAACCTTCT 620
 |||
 Db 10 LeuLeuLeuThrValThrSer 16

RESULT 42

ABB80898
 ID ABB80898 standard; Protein: 98 AA.

XX ABB80898;

XX 08-OCT-2002 (first entry)

XX Murine eotaxin polypeptide fragment.

XX Eotaxin: eosinophil; chemotaxis; cytostatic; antiinflammatory; cardiant;
 KW antiallergic; immunosuppressive; antiasthmatic; antiparasitic; histamine;
 KW dermatological; vasotropic; gene therapy; antianaphylactic; mouse.

XX Mus musculus.

PN US6403782-B1.

PD 11-JUN-2002.

XX 04-AUG-1999; 99US-0366887.

XX 22-JUN-1995; 95US-000449P.

PR 01-SEP-1995; 95US-0522713.

XX (HARD) HARVARD COLLEGE.

PA (GEHO) GEN HOSPITAL CORP.

XX Luster AD, Leder P, Rothenberg M, Garcia E;

DR WPI; 2002-565447/60.

XX New DNA encoding murine, guinea pig or human eotaxin polypeptides,

PT useful for treating inflammation and tumorigenesis and in anticancer

PT gene therapy -

XX Disclosure; Fig 3B; 42pp; English.

XX The invention relates to polynucleotides encoding murine, guinea pig or
 CC human eotaxin polypeptides. The eotaxin polynucleotides are useful for
 CC modulating eosinophil chemotaxis, for increasing eosinophil chemotactic
 CC events, and for improving prognosis with tumours in patients. They are
 CC also useful for treating inflammation and tumourigenesis, and for
 CC reducing inflammation and cytotoxic damage caused by eosinophils, for
 CC e.g. during asthmatic reactions, eosinophilic pneumonia and allergic
 CC diseases, inflammatory bowel diseases, atopic dermatitis, urticaria,
 CC vasculitis, parasitic infections and eosinophil cardiac diseases. The
 CC eotaxin polynucleotides are also useful for modulating histamine release
 CC by modulating eotaxin activity or expression during anaphylaxis,
 CC urticaria and allergic reactions. They are useful for detecting and
 CC monitoring eosinophil mediating conditions, and in anti-cancer gene
 CC therapy. The present sequence represents the murine eotaxin fragment.

XX Sequence 98 AA;

Alignment Scores:

Pred. No.: 293

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.92%

Length: 98

Matches: 7

Conservative: 0

Indels: 0

Gaps: 0

US-09-817-318-1 (1-780) x ABB80898 (1-98)

OY 640 TTGTTATTCAGCTACTCT 620

Db 10 LeuLeuLeuThrValThrSer 16

RESULT 43

AAU59212
ID AAU59212 standard; Protein: 99 AA.

AC AAU59212;

DT 27-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #20108.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;

KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;

KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;

KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX OS

XX PN WO200181581-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12865.

XX PR 21-APR-2000; 2000US-199047P.

XX PR 02-JUN-2000; 2000US-208841P.

XX PR 07-JUL-2000; 2000US-216747P.

XX PA (CORI-) CORIXA CORP.

XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX DR WPI: 2001-616774/71.

XX DR N-PSDB; AASS9601.

XX PT Propionibacterium acnes polypeptides and nucleic acids useful for

XX PT vaccinating against and diagnosing infections, especially useful for

XX PT treating acne vulgaris -

XX PS Example 1: SEQ ID NO 20407; 1069pp; English.

XX XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic

CC polypeptides. The proteins and their associated DNA sequences are used in

CC the treatment, prevention and diagnosis of medical conditions caused by

CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,

CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

CC P. acnes is also involved in infections of bone, joints and the central

CC nervous system, however it is particularly involved in the inflammatory

CC lesions associated with acne vulgaris. A method for detecting the

CC presence or absence of P. acnes in a patient comprises contacting a

CC sample with a binding agent that binds to the proteins of the invention

CC and determining the amount of bound protein in the sample. The

CC polypeptides may be used as antigens in the production of antibodies

CC specific for P. acnes proteins. These antibodies can be used to

CC downregulate expression and activity of P. acnes polypeptides and

CC therefore treat P. acnes infections. The antibodies may also be used as

CC diagnostic agents for determining P. acnes presence, for example, by

CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX XX

SO Sequence 99 AA:

Alignment Scores: 293 Length: 99

Pred. No.: 7 Matches: 7

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.92%

Db: 22 Gaps: 0

US-09-817-318-1 (1-780) x AAU59212 (1-99)

OY 162 GATTAGTGAGCTGCTATTA 142

Db 24 AspleuValLysLeuLeuLeu 30

RESULT 44

AAO07453
ID AAO07453 standard; Protein: 100 AA.

AC AAO07453;

DT 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 21345.

XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX PN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US04927.

XX PR 28-FEB-2000; 2000US-0515126.

XX PR 18-MAY-2000; 2000US-0577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI: 2001-514838/56.

XX DR N-PSDB; AAI87384.

XX PT The invention relates to human polynucleotides (AAI79941-AAI93841) and

XX PT the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to

XX PT cytokine, cell proliferation or cell differentiation or which may induce

XX PT production of other cytokines in other cell populations. The

XX PT polynucleotides and polypeptides are useful in gene therapy, vaccines or

XX PT peptide therapy. The polypeptides have various cytokine-like activities,

XX PT e.g. stem cell growth factor activity, haematopoiesis regulating

XX PT activity, tissue growth factor activity, immunomodulatory activity and

XX PT activin/inhibin activity and may be useful in the diagnosis and/or

XX PT treatment of cancer, leukaemia, nervous system disorders, arthritis and

XX PT inflammation.

XX PT Note: The sequence data for this patent did not form part of the printed

XX PT specification, but was obtained in electronic format directly from WIPO

XX PT at ftp.wipo.int/pub/published_pct_sequences.

XX XX

SO Sequence 100 AA:

Alignment Scores: 293 Length: 100

Pred. No.: 7 Matches: 7

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.92%

Indels: 0

DB: 22 Gaps: 0

US-09-817-318-1 (1-780) x AA007453 (1-100)

QY 649 AACATACTTGTATTGACA 629
 |||||

Db 31 Asn1eThrLeuLeuThr 37

RESULT 45

ABP31587

ID ABP31587 standard; Protein: 104 AA.

AC ABP31587;

XX

DT 08-JUL-2002 (first entry)

XX

DE Human ORF560 protein, SEQ ID NO:1120.

XX

KW Human; ORF: open reading frame; ORFX: drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; hematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokine; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristics; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vunerary;
 KW vasotropic; antiporiatic; antidiabetic; cyostatic; nootropic;
 KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antihypertoid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX

OS Homo sapiens.

XX

PN WO200190366-A2.

XX

PD 29-NOV-2001.

XX

PF 24-MAY-2001; 2001WO-US17076.

XX

PR 24-MAY-2000; 2000US-206690P.

XX

PA (CURA-) CUBAGEN CORP.

XX

PI Leach MD, Shimkets RA;

XX

DR MPI: 2002-106200/14.

XX

DR N-PSDB: ABN75613.

XX

PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation

XX

PS Claim 10; Page 546; 2508pp; English.

XX

CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening for modulators of ORFX expression or
 CC activity, and methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, hematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokine activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antiinfective activity, and may also be involved in the determination

CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts. In the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases.

XX SQ Sequence 104 AA;

Alignment Scores:

Pred. No.:	292	Length:	104
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	23	Gaps:	0

US-09-817-318-1 (1-780) x ABP31587 (1-104)

QY 398 ACTCATTTGTTAAGTTT 418
 |||||

Db 52 Thr1sLeuLeuThrSerPhe 58

Search completed: February 4, 2003, 07:21:52
 Job time : 50.5 secs

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 4, 2003, 07:17:28 : Search time 15.5 Seconds
(without alignments)
4174.392 Million cell updates/sec

Title: US-09-817-318-1
Perfect score: 245
Sequence: 1 aattactgtctcttaag.....taagagcaaaaaaaaaa 780

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Word size: 1

Total number of hits satisfying chosen parameters: 225614

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+o2p model -DEV=x1p
-O=/cgn2_1/USPTO.spool/US09817318/runal_04022003_071721_6612/app-query.fasta.1.967
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=resp -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
-DLOCALIGN=200 -THR.SCOR=quality -THR.MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFMT=plc
-NOR-ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=US09817318 -ECGN_1_1_13 -funal_04022003_071721_6612 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WALR.TIMEOUT=30 -THREDS=1 -XGAPOP=60 -XGAPEXT=60 -FCGAPOP=6 -FCGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	3.3	528	1	ASMA4_YEAST
2	8	3.3	607	1	PEPF_MYCE
3	7	2.9	97	1	EOTA_MOUSE
4	7	2.9	100	1	NULM_PHYIN
5	7	2.9	103	1	NIEW_TRISI
6	7	2.9	105	1	THIL_DICDI
7	7	2.9	117	1	VIL7_HAEDU
8	7	2.9	117	1	LY6F_MOUSE
9	7	2.9	171	1	PA1A_BACSU
10	7	2.9	173	1	RPOE_BACSU
11	7	2.9	174	1	YPUF_BACSU
12	7	2.9	219	1	CIDA_HUMAN
13	7	2.9	219	1	REPP2_SCHRO
14	7	2.9	220	1	Y069_GAEBL
15	7	2.9	245	1	PHOS_BOVIN
16	7	2.9	245	1	PHOS_CANFA
17	7	2.9	283	1	CHER_BORBU
18	7	2.9	283	1	PSTA_RHILU

19	7	2.9	312	1	KRAW_BUCAP	085295 buchnera ap
20	7	2.9	314	1	REBN_SALTY	p26403 salmonella
21	7	2.9	328	1	HA1Q_MOUSE	p14428 mus musculus
22	7	2.9	332	1	HRDD_STYF	060012 streptomyc
23	7	2.9	333	1	MDHC_HUMAN	p40925 homo sapien
24	7	2.9	333	1	MDHC_MOUSE	p14152 mus musculus
25	7	2.9	355	1	C3X1_HUMAN	p49238 homo sapien
26	7	2.9	368	1	HA1D_HUMAN	p01902 mus musculus
27	7	2.9	368	1	HA1W_MOUSE	p03391 mus musculus
28	7	2.9	369	1	HA1B_MOUSE	p01901 mus musculus
29	7	2.9	369	1	HA1K_MOUSE	p04223 mus musculus
30	7	2.9	371	1	CYB_CANAS	048023 candoia asp
31	7	2.9	385	1	O46A_DROME	p81919 drosophila
32	7	2.9	411	1	Y360_MYCME	049426 mycoplasma
33	7	2.9	415	1	AMSJ_ERYAN	046637 erwinia amy
34	7	2.9	435	1	POTE_HAELN	p44766 haemophilus
35	7	2.9	447	1	G6P1_LACIA	p81181 lactococcus
36	7	2.9	453	1	YKK8_YEAST	p34252 saccharomyc
37	7	2.9	459	1	N04M_HUMAN	p03905 homo sapien
38	7	2.9	460	1	N04M_HUMAN	09miy1 brachydanio
39	7	2.9	461	1	PRTC_RAT	p31394 rattus norv
40	7	2.9	463	1	FMNL_HUMAN	095466 homo sapien
41	7	2.9	475	1	AP54_YEAST	000776 saccharomyc
42	7	2.9	486	1	YDE5_SCHRO	010439 schizosacch
43	7	2.9	513	1	VGA_BPPHX	p03631 bacterioph
44	7	2.9	519	1	SC59_YEAST	p20048 saccharomyc
45	7	2.9	522	1	VGA_BP513	p07928 bacterioph

ALIGNMENTS

RESULT 1

ASMA4_YEAST
ID ASMA4_YEAST STANDARD: PRT: 528 AA.

AC Q05166: Q12456;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ASMA4 protein.

GN ASMA4 OR YDL088C OR D2420.

OS Saccharomyces cerevisiae (Baker's yeast).

CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

CC NCB1_TaxID=4932;

RN NCB1

RP [1]

SEQUENCE FROM N.A.

RX MEDLINE=95166178; PubMed=7862092;

RA Glot L., Simon M., Dubois C., Faye G.;

RT "Suppressors of thermosensitive mutations in the DNA polymerase delta

gene of Saccharomyces cerevisiae.";

RL Mol. Gen. Genet. 246:212-222(1995).

RN [2]

SEQUENCE FROM N.A.

RC STRAIN=S288c / FY1679;

RA Boskovjc J., Saiz J.E., Soler-Mira A., Garcia-Cantalejo J.,

Revenilla J.L., Jimenez A., Ballesta J.P.G., del Rey F., Remacha M.;

RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RA Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.

RL -I- MISCELLANEOUS: SUPPRESSOR OF THERMOSENSITIVE MUTATIONS IN THE DNA

POLYMERASE DELTA GENE (POL3).

CC -I- SIMILARITY: TO YEAST YMR153W.

CC

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DR EMBL: X76709; CAA54130.1; -
DR EMBL: X95644; CAA64923.1; -
DR EMBL: 274136; CAA98654.1; -
DR SGD: S0002246; ASW4.
FT DOMAIN 38 46 POLY-GLN.
FT 84 87 POLY-ASN.
FT CONFLICT 114 114 F->L (IN REF. 1).
FT CONFLICT 446 528 PAGHAGNPTNISPPIVANSPNKRLVDIDGKLPFMONAGPNS
NIPNLRLNLESKMRQOEAKRYRNPAGFTHKLSNLPFGMND
L->LPMVLYCOQFOYO (IN REF. 1).
SQ SEQUENCE 528 AA; 58793 MW; 84FE1F07FC1B0173 CRC64;
Alignment Scores:
Pred. No.: 6.98 Length: 528
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 8
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 1 Gaps: 0
US-09-817-318-1 (1-780) x ASW4_YEAST (1-528)
QY 670 ATAATTCATTACTGAGCAATTC 693
Db 170 ILeasSerLeuSerAspPhe 177
RESULT 2
ID PEPF_MYCGE STANDARD; PRT; 607 AA.
AC P47429;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oligendopeptidase F homolog (EC 3.4.24.-).
GN PEPF OR MG183.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann J.R., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Luster T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium.";
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 10-111 FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
RN [3]
CC -1- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U39697; AAC71402.1; -
CC DR EMBL: U02198; AAD12484.1; -
CC DR MEROPS: M03_UBB; -
CC TIGR: MG183; -

DR InterPro: IPR004438; PePF.
DR InterPro: IPR001567; Peptidase_M3.
DR InterPro: IPR000130; Zn_MPeptidse.
DR Pfam: PF01432; Peptidase_M3; 1.
DR TIGRFAMS: TIGR00181; PePF; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Complete proteome.
FT METAL 384 384 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 385 385 BY SIMILARITY.
FT METAL 388 388 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 391 391 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 607 AA; 70869 MW; 47IDFF73A4ED7 CRC64;
Alignment Scores:
Pred. No.: 6.8 Length: 607
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 8
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 1 Gaps: 0
US-09-817-318-1 (1-780) x PEPF_MYCGE (1-607)
QY 150 TTGCTATTGCTATTATGACTA 127
Db 419 LeuLeuLeuCysTyrTyrGluLeu 426
RESULT 3
ID EOTL_MOUSE STANDARD; PRT; 97 AA.
AC P48298;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A1) (CCL11) (Eosinophil
DE chemotactic protein).
GN SCY11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=96004658; PubMed=7568052;
RA Rothenberg M.E., Luster A.D., Leder P.;
RT "Murine eotaxin: an eosinophil chemoattractant inducible in
RT endothelial cells and in interleukin 4-induced tumor suppression.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:8960-8964(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=96158746; PubMed=8574847;
RA Gonzalo J.-A., Jia G.-O., Aguirre V., Friend D., Coyle A.J.,
RA Jenkins N.A., Lin G.-S., Katz H., Lichtman A., Copeland N.G., Kopf M.,
RA Gutierrez-Ramos J.-C.;
RT "Mouse eotaxin expression parallels eosinophil accumulation during
RT lung allergic inflammation but it is not restricted to a Th2-type
RT response.";
RL Immunity 4:1-14(1996).
RN [3]
CC -1- FUNCTION: IN RESPONSE TO THE PRESENCE OF ALLERGENS, THIS PROTEIN
CC DIRECTLY PROMOTES THE ACCUMULATION OF EOSINOPHILS (A PROMINENT
CC FEATURE OF ALLERGIC INFLAMMATORY REACTIONS), BUT NOT
CC LYMPHOCYTES, MACROPHAGES OR NEUTROPHILS.
CC -1- TISSUE SPECIFICITY: EXPRESSED CONSTITUTIVELY IN THE THYMUS.
CC -1- TISSUE SPECIFICITY: EXPRESSED CONSTITUTIVELY IN THE THYMUS.
CC EXPRESSION INDUCIBLE IN THE LUNG (TYPE I ALVEOLAR EPITHELIAL
CC CELLS), INTESTINE, HEART, SPLEEN, KIDNEY.
CC -1- INDUCTION: BY INTERFERON GAMMA AND LIPOLYSACCHARIDE (LPS).
CC -1- SIMILARITY: BELONGS TO THE INTERFERON BETA FAMILY (SMALL CYTOKINE
CC C-C) (CHEMOKINE CC).
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DR EMBL: U26426; AAC52256.1; -
 DR EMBL: U40672; AAA99776.1; -
 DR HSSP: P51671; LEOT.
 DR MGD: MG1:103576; Scyall.
 DR InterPro: IPR000827; CC_Chemkine_sml.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR Pfam: PF00048; IL8; 1.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
 KW Eosinophil; Cytokine; Chemotaxis; Glycoprotein; Signal;
 KM Inflammatory response.
 FT SIGNAL 1 23
 FT CHAIN 24 97
 FT DISULFID 32 57
 FT DISULFID 33 73
 FT CARBOHYD 94 94
 SQ SEQUENCE 97 AA; 10893 MW; 36C9812107FC6CA7 CRC64; (BY SIMILARITY).

Alignment Scores:
 Pred. No.: 103 Length: 97
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x EOTA_MOUSE (1-97)

OY 640 TTGTTATTGACAGTACTTCT 620
 ||||||||||||||||
 Db 10 LeuLeuLeuThrValThrSer 16

RESULT 4
 NULM_PHYIN STANDARD; PRT; 100 AA.
 ID NULM_PHYIN
 AC Q37598;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
 GN NAD4L OR NAD4L.
 OS Phytophthora infestans (potato late blight fungus).
 OC Mitochondrion.
 OC Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
 OC Phytophthora.
 OX NCBL_TaxID=4787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 16981 / West Virginia 4;
 RA Lang B.F., Forget L.;
 RT "The mitochondrial genome of *Phytophthora infestans*."
 RL (in) O'Brien S.J. (eds.);
 RL Genetic maps, pp.3:133-135, Cold Spring Harbor Laboratory Press,
 RN New-York (1992).
 RP [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN-ATCC 16981 / West Virginia 4;
 RA Chesnick J.M., Tuxbury K., Coleman A., Burger G., Lang B.F.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -----
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DR EMBL: U17009; AAF24790.1; -
 DR EMBL: U54634; AAB00440.1; -
 DR InterPro: IPR003215; NADH_dh_ubiq1.
 DR InterPro: IPR001133; Oxidored4L.
 DR InterPro: IPR003214; Oxidored4L.
 DR Pfam: PF00420; Oxidored_q2; 1.
 DR ProDom: PD002107; NADH_dh_ubiq1; 1.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ SEQUENCE 100 AA; 11277 MW; 199092C0874BCB15 CRC64;

Alignment Scores:
 Pred. No.: 103 Length: 100
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x NULM_PHYIN (1-100)

OY 114 TATAAATTAACCTACTCTCA 94
 ||||||||||||||||
 Db 93 TyrIlysIleAsnLeuLeuSer 99

RESULT 5
 NIFW_TRIS1 STANDARD; PRT; 103 AA.
 ID NIFW_TRIS1
 AC O9KJL4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nitrogenase stabilizing/protective protein nifw.
 GN NIFW.
 OS Trichodesmium sp. (strain IMS101).
 OC Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium.
 OX NCBL_TaxID=57878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dominic B., Zani S., Chen Y.-B., Mellon M.T., Zehr J.P.;
 RT "Organization of the nif genes of the nonheterocystous cyanobacterium
 RT Trichodesmium sp. IMS101."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May protect the nitrogenase Fe-Mo protein from oxidative
 CC damage (By similarity).
 CC -!- SUBUNIT: Homotrimer; associates with nifd (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE NIFW FAMILY.
 CC -----
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DR EMBL: AF167538; AAF82643.1; -
 DR InterPro: IPR004893; Nifw.
 DR Pfam: PF03206; Nifw; 1.
 KW Nitrogen fixation.
 SQ SEQUENCE 103 AA; 11819 MW; BE423C1E4309D2A6 CRC64;

Alignment Scores:
 Pred. No.: 102 Length: 103
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x NIFW_TRIS1 (1-103)

OY 542 ACAGTCATGTAATGATTG 522
 DB 28 ThrValAsnValAsnArgLeu 34

RESULT 6
 TH1L_DICDI STANDARD: PRT; 105 AA.
 ID TH1L_DICDI
 AC P29445;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Thioresdoxin 1.
 GN TRXA OR TRX1.
 OS Dictyostellium discoideum (slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelidia; Dictyostellium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92250653; PubMed=1577820;
 RA Wettelauer B., Jacquot J.-P., Veron M.;
 RT "Thioredoxins from Dictyostellium discoideum are a developmentally
 regulated multigene family";
 RL J. Biol. Chem. 267:9895-9904(1992).
 CC
 CC -!- FUNCTION: Participates in various redox reactions through the
 reversible oxidation of its active center dithiol to a disulfide
 and catalyses dithiol-disulfide exchange reactions.
 CC
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 CC
 CC EMBL: M91384; AAA3258.1; -
 DR PIR: A46264; A46264.
 DR HSSP: P10599; 1ERV.
 DR DICTYDB: D05029; trxa.
 DR InterPro: IPR000063; Thiores.
 DR Pfam: PF00085; Thioresdoxin.
 DR PRINTS: PR00421; THIOREDOXIN.
 DR PROSITE: PS00194; THIOREDOXIN, 1.
 KW Redox-active center; Electron transport; Multigene family.
 FT DISULFID 32 35 REDOX-ACTIVE (BY SIMILARITY).
 SQ SEQUENCE 105 AA; 11926 MW; 0BC12C2867CEB1F5 CRC64;

Alignment Scores:
 Pred. No.: 102 Length: 105
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x TH1L_DICDI (1-105)

OY 686 CTCAGTAATGATTATTCAC 666
 DB 45 LeuSerAsnGluPheIleThr 51

RESULT 7
 Y117_HAEDU STANDARD: PRT; 117 AA.
 ID Y117_HAEDU
 AC O30825;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Hypothetical protein HYPO117.
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.

OX NCBI_TaxID=730;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=35000;
 RA San Mateo L.R., Toffer K.L., Kawula T.H.;
 RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 CC
 CC -!- SIMILARITY: BELONGS TO THE UPF0076 (ORF114) FAMILY.
 CC
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 CC
 CC EMBL: AF017750; AAC46218.1; -
 DR InterPro: IPR000543; Y3GF-like.
 DR Pfam: PF01042; UPF0076; 1.
 DR PROSITE: PS01094; UPF0076; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 117 AA; 13252 MW; BB3FB8C4827940B2 CRC64;

Alignment Scores:
 Pred. No.: 99.8 Length: 117
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x Y117_HAEDU (1-117)

OY 163 ACATTGATGAGTGTCTATT 143
 DB 10 ArgPheSerGluValAlaIle 16

RESULT 8
 LY6F_MOUSE STANDARD: PRT; 134 AA.
 ID LY6F_MOUSE
 AC P35460;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lymphocyte antigen Ly-6F.1 precursor.
 GN LY6F.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver.
 RX MEDLINE=93294293; PubMed=8515066;
 RA Fleming T.J., O'Huigin C., Malek T.R.;
 RT "Characterization of two novel Ly-6 genes. Protein sequence and
 potential structural similarity to alpha-bungarotoxin and other
 neurotoxins";
 RL J. Immunol. 150:5379-5390(1993).

-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 similarity).
 CC
 CC -!- SIMILARITY: CONTAINS 1 UPAR/LY6 DOMAIN.
 CC
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 CC
 CC EMBL: X70922; CAA50270.1; -
 DR EMBL: X70918; CAA50270.1; JOINED.


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DR EMBL: X70919: CAAS0270.1; JOINED.
DR MGD; MGI:109441; LY6f.
DR InterPro: IPR001526; LY6_UPAR.
DR Pfam: PF00021; UPAR_LY6; 1.
DR SMART: SM00134; LY; 1.
DR PROSITE: PS00983; LY6_UPAR; 1.
KW T-cell; Signal; Antigen; Multigene family; GPI-anchor.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 219 LYMPHOCYTE ANTIGEN LY-6F.1.
FT PROPEP 27 134 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 27 119 UPAR/LY6.
FT DISULFID 29 53 BY SIMILARITY.
FT DISULFID 32 41 BY SIMILARITY.
FT DISULFID 46 74 BY SIMILARITY.
FT DISULFID 98 98 BY SIMILARITY.
FT LIPID 119 119 GPI-ANCHOR (POTENTIAL).
SO SEQUENCE 134 AA; 14599 MW; 3F9DD32FA9183CA CRC64;

Alignment Scores:
Pred. No.: 97.3 Length: 134
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x LY6F_MOUSE (1-134)

OY 701 GTTTAATTCCTCGTGTGTA 721
|||||
Db 11 ValleuleleuValVal 17

RESULT 9
PAIA_BACSU STANDARD; PRT; 171 AA.
ID PAIA_BACSU STANDARD; PRT; 171 AA.
AC P21340; O32112;
DT 01-MAY-1991 (Rel. 18, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protease synthase and sporulation negative regulatory protein PAI 1.
GN PAIA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.
RC STRAIN=168 / DB104;
RX MEDLINE=90202692; PubMed=2108124;
RA Honjo M., Nakayama A., Fukazawa K., Kawamura K., Ando K., Hori M.,
RA Furutani Y.;
RT "A novel Bacillus subtilis gene involved in negative control of
RT sporulation and degradative-enzyme production.";
RL J. Bacteriol. 172:1783-1790(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Aaevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borst R., Boursier L., Brans A., Braun M., Britnell S.C., Bron S.,
RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Enlilen S.D., Emmertson P.T.,
RA Ertlan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Frits C., Fujita M., Fujita Y., Fuma S., Gallizi A., Galleron N.,
RA Gilm S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Kletter-Bianchini M., Klein C.,
RA Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapius A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
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RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Poterlik S., Prescott A.M.,
RA Prescan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadleir Y.,
RA Sato T., Scanlan E., Schleich S., Schreier R., Scifone F.,
RA Sekiguchi J., Sekowska S., Serró S.J., Serró P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vanlier F., Vassarotti A.,
RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzengraber T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumschein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
CC -1- FUNCTION: INVOLVED IN NEGATIVE CONTROL OF SPOULATION AND
CC DEGRADATIVE-ENZYME PRODUCTION.
CC -1- SIMILARITY: STRONG. TO L.DELBRUECKII HYPOTHETICAL PROTEIN IN PEPI
CC 3'REGION (AC P46543). SOME, TO M.TUBERCULOSIS RV2669.
CC -----
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CC -----
DR EMBL: M36471; AAA22638.1; -.
DR EMBL: 299120; CAB15205.1; -.
DR PIR: A35145; A35145.
DR Subtilist; BG10695; paia.
DR InterPro: IPR000182; GCN5acetyltransf.
DR Pfam: PF00583; Acetyltransf; 1.
KW DNA-binding; Transcription regulation; Repressor; sporulation;
KM Complete proteome.
FT INT MET 0 0
FT DNA_BIND 97 121 H-T-H MOTIF.
FT CONFLICT 26 26 T->I (IN REF. 1).
SO SEQUENCE 171 AA; 19883 MW; DB5EB6869647C9D CRC64;

Alignment Scores:
Pred. No.: 93.1 Length: 171
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x PAIA_BACSU (1-171)

OY 504 TCTTCCAAAGCATGGGCTT 484
|||||
Db 100 Serpheginlyshisglyleu 106

RESULT 10
RPOE_BACSU STANDARD; PRT; 173 AA.
ID RPOE_BACSU STANDARD; PRT; 173 AA.
AC P12464;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase delta subunit (RNAP delta factor).
GN RPOE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88329737; PubMed=2843435;
RA Lampe M., Blinle C., Schmidt R., Losick R.;
RT "Cloned gene encoding the delta subunit of Bacillus subtilis RNA
```

RT polymerase.";
 RL Gene 67:13-19(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=98015417; PubMed=9353933;
 RA Prescan E., Moszer I., Boursier L., Cruz Ramos H.C., De la Fuente V.,
 RA Hullo M.-F., Lelong C., Schleich S., Sekowska A., Song B.H.,
 RA Villani G., Kunst F., Danchin A., Glaser P.;
 RT "The Bacillus subtilis genome from gerBC (311 degrees) to l1cR (334
 RT degrees)." ;
 RL Microbiology 143:3313-3328(1997).
 RN [3]
 RP SEQUENCE OF 143-173 FROM N.A.
 RC STRAIN-168 / JH642;
 RX MEDLINE=88314920; PubMed=2457578;
 RA Trach K., Chapman J.W., Pigot P., Lecocq D., Hoch J.A.;
 RT "Complete sequence and transcriptional analysis of the spo0F region
 RT of the Bacillus subtilis chromosome." ;
 RL J. Bacteriol. 170:4194-4208(1988).
 RN [4]
 RP CHARACTERIZATION
 RX MEDLINE=95404613; PubMed=7545758;
 RA Lopez de Saro F.J., Woody A.Y., Helmann J.D.;
 RT "Structural analysis of the Bacillus subtilis delta factor: a protein
 RT polyanion which displaces RNA from RNA polymerase." ;
 RL J. Mol. Biol. 252:189-202(1995).
 RN [5]
 RP CHARACTERIZATION
 RX MEDLINE=99269144; PubMed=10336502;
 RA Lopez de Saro F.J., Yoshikawa N., Helmann J.D.;
 RT "Expression, abundance, and RNA polymerase binding properties of the
 RT delta factor of Bacillus subtilis." ;
 RL J. Biol. Chem. 274:15953-15958(1999).
 CC -1- FUNCTION: Participates in both the initiation and recycling phases
 CC of transcription. In the presence of the delta subunit, RNAP
 CC displays an increased specificity of transcription, a decreased
 CC affinity for nucleic acids, and an increased efficiency of RNA
 CC synthesis because of enhanced recycling. May function in sigma
 CC factor switching. It displaces RNA bound to RNA polymerase in a
 CC binary complex.
 CC -1- SUBUNIT: RNAP is composed of a core of 2 alpha, a beta and a beta'
 CC subunits. The core is associated with a delta subunit and one of
 CC several sigma factors.
 CC -1- SIMILARITY: BELONGS TO THE RPOE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M21677; AAA22710.1; -
 DR EMBL: 249782; CAA89869.1; -
 DR EMBL: M22039; AAA16800.1; -
 DR EMBL: 299123; CAA15744.1; -
 DR PIR: JTO302; JTO302.
 DR PIR: H32354; H32354.
 DR Subtilisin; BG10409; rPOE.
 KW DNA-directed RNA polymerase; Transcription; Complete proteome.
 FT DOMAIN 107 173
 FT ASP/GLU-RICH (ACIDIC).
 SQ SEQUENCE 173 AA; 20399 MW; 0F5818802654417D CRC64;

Alignment Scores:
 Pred. No.: 92.9 Length: 173
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x RPOE_BACSU (1-173)
 QY 760 GTAAGCGCAAAAAAAAAA 780
 DB 95 VALLYSALATSLYSLYSLYS 101
 RESULT 11
 YPUF_BACSU
 ID YPUF_BACSU STANDARD; PRT; 174 AA.
 AC P17617;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein ypuF (ORF6).
 GN ypuF.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxId=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / Marburg;
 RX MEDLINE=95020538; PubMed=7934829;
 RA Sorokin A.V., Zumstein E., Azevedo V., Ehrlich S.D., Serror P.;
 RT "The organization of the Bacillus subtilis 168 chromosome region
 RT between the spoVA and serA genetic loci, based on sequence data." ;
 RL Mol. Microbiol. 10:385-395(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / SHGW;
 RA Mironov V.N.;
 RT Thesis (1989), USSR Academy of Sciences, Russia.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Berrero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Bortiss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Ertan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritsch C., Fujita M., Fujita Y., Fuma S., Gallizzi A., Galleron N.,
 RA Gim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Kjaer-Blanchard M., Klein C.,
 RA Kobayashi Y., Koelter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Portwilk S., Prescott A.M.,
 RA Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,
 RA Sekiyuchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Takakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Toseato V., Uchiyama S., Vandenbol M., Vannier F., Vasseroiti A.,
 RA Viari A., Wambuit R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis." ;
 RL Nature 390:249-256(1997).
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CC -----
DR EMBL: I092228; AAA67486.1; -
DR EMBL: X51510; CAA35883.1; -
DR EMBL: Z99116; CAB14255.1; -
DR PIR: S45548; S45548.
DR Subtilist: BG10523; YPUF.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 174 AA; 21021 MW; 2D969CFAFCB7EBAE CRC64;

Alignment Scores:
Pred. No.: 92.8 Length: 174
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x YPUF_BACSU (1-174)
QY 603 TTATCTATATCTTTTGATT 583
Db 141 LeuSerAsnIlePheIleu 147

RESULT 12
CIDA_HUMAN STANDARD; PRT; 219 AA.
AC 060543;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell death activator CIDE-A (Cell death-inducing DFFA-like effector
A).
GN CIDEA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=98232498; PubMed=9564035;
RA Inohara N., Koseki T., Chen S., Wu X., Nunez G.;
RT "CIDE, a novel family of cell death activators with homology to the 45
RL KDA subunit of the DNA fragmentation factor.";
RL EMBO J. 17:2526-2533(1998).
CC -1- FUNCTION: ACTIVATES APOPTOSIS.
CC -1- SUBUNIT: INHIBITED BY DFFB.
CC -1- SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
CC -----
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CC -----
DR EMBL: AF041378; AAC34987.1; -
DR HSP: Q50HD4; ID4B.
DR Genew: HGNC:1976; CIDEA.
DR MIM: 604440; -
DR InterPro: IPR003508; CAD.
DR Pfam: PF02017; CIDE-N; 1.
DR SMART: SM00266; CAD; 1.
KW Apoptosis.
FT DOMAIN 33 110 CIDE-N.
SQ SEQUENCE 219 AA; 24686 MW; 05F704823CE71C0E CRC64;

Alignment Scores:
Pred. No.: 88.9 Length: 219
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

```

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Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x CIDA_HUMAN (1-219)
QY 281 ACAAGAGGCTGCTTTTACA 301
Db 22 ThrIysArgValIleuPheThr 28

RESULT 13
REP2_SCHPO STANDARD; PRT; 219 AA.
ID REP2_SCHPO
AC 009824;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Transcriptional activator protein rep2.
DE REP2 OR SPBC2F12.11C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae.
OX Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RX MEDLINE=96030785; PubMed=7588609;
RA Nakashima N., Tanaka K., Sturm S., Okayama H.;
RT "Fission yeast Rep2 is a putative transcriptional activator subunit
RL for the cell cycle 'start' function of Rep2-Cdc10.";
RL EMBO J. 14:4794-4802(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Felwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welfjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wandutt R., Purnelle B.,
RA Gofeu A., Cadieu E., Dreano S., Gloux S., Delaure V., Motlier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: TRANSCRIPTIONAL ACTIVATOR WHICH INTERACTS WITH THE MCB
CC BINDING SUBUNIT COMPLEX FORMED BY REP2 AND CDC10. REP2 IS REQUIRED
CC FOR THE MITOTIC CELL CYCLE START.
CC -1- SIMILARITY: TO REP1.
CC -----
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DR EMBL: X91044; CAA62504.1; -
 DR EMBL: Z97211; CAB10158.1; -
 DR TRANSFAC: T04219; -
 DR InterPro: IPR000822; znf.C2H2.
 DR Pfam: PF00096; zf-C2H2; 1.
 KM Transcription regulation; Activator; Zinc-finger; Metal-binding;
 KW Phosphorylation; Mitosis; Cell cycle.
 FT ZN_FING 177 197 POTENTIAL.
 SQ SEQUENCE 219 AA; 24668 MW; 77F1IA406E722656 CRC64;

Alignment Scores:

Pred. No.:	88.9	Length:	219
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	1	Gaps:	0

US-09-817-318-1 (1-780) x REP2_SCHPO (1-219)

OY 418 TCTTGTGAGTTCCTTGCC 438

DB 42 SetServerSerPheala 48

RESULT 14

ID Y069_CAEEL STANDARD; PRT; 220 AA.

AC P34608;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical 23.9 kDa protein ZK1098.9 in chromosome III.

GN ZK1098.9.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-Bristol N2; PubMed-7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,

RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,

RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,

RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,

RA Sims M., Smailton N., Smith A., Smith M., Sonnenhammer E., Staden R.,

RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,

RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,

RA Wohldman P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans";

RL Nature 368:32-38(1994).

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CC -----

DR EMBL: Z22176; CAA80138.1; -

DR PIR: S40931; S40931.

DR WormPep: ZK1098.9; CE00371.

KW Hypothetical protein.

SQ SEQUENCE 220 AA; 23880 MW; 3F321A431A6E3F84 CRC64;

Alignment Scores:

Pred. No.:	88.8	Length:	220
Score:	7.00 <td>Matches:</td> <td>7</td>	Matches:	7

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x Y069_CAEEL (1-220)

OY 546 TGCATTGATGCTAGATGTT 566

DB 183 Cysillevalleuanspyal 189

RESULT 15

PHOS_BOVIN

ID PHOS_BOVIN STANDARD; PRT; 245 AA.

AC P19632; P20940; Q28160;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Phosducin (PHD) (33 kDa phototransducing protein) (MEKA protein).

GN PDC.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE, AND SEQUENCE OF 228-245 FROM N.A.

RC TISSUE-Retina;

RA MEDLINE-90368806; PubMed-2203790;

RA Lee R.H., Fowler A., McGinnis J.F., Lolley R.N., Craft C.M.;

RT "Amino acid and cDNA sequence of bovine phosducin, a soluble

phosphoprotein from photoreceptor cells";

RL J. Biol. Chem. 265:15867-15873(1990).

RN [2]

RP SEQUENCE FROM N.A.

RC MEDLINE-89364083; PubMed-2770450;

RA Kuo C.-H., Akiyama M., Miki N.;

RT "Isolation of a novel retina-specific clone (MEKA cDNA) encoding a

photoreceptor soluble protein";

RL Brain Res. Mol. Brain Res. 6:1-10(1989).

RN [3]

RP SEQUENCE OF 8-245 FROM N.A.

RC TISSUE-Retina; and Pineal gland;

RA MEDLINE-91007277; PubMed-2210381;

RA Abe T., Nakabayashi H., Tamada H., Takagi T., Sakurai S., Yamaki K.,

RA Shiohara T.;

RT "Analysis of the human, bovine and rat 33-kDa proteins and cDNA in

retina and pineal gland";

RL Gene 91:209-215(1990).

RN [4]

RP PHOSPHORYLATION OF SER-73.

RC MEDLINE-90368805; PubMed-2394752;

RA Lee R.H., Brown B.M., Lolley R.N.;

RT "Protein kinase A phosphorylates retinal phosducin on serine 73 in

situ";

RL J. Biol. Chem. 265:15860-15866(1990).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH G-BETA AND

G-GAMMA.

RA MEDLINE-98416696; PubMed-9739091;

RA Loew A., Ho Y.K., Blundell T., Bax B.;

RT "Phosducin induces a structural change in transducin beta gamma";

RL Structure 6:1007-1019(1998).

CC -----

CC -!- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL

PHOTOPHOSPHORYLATION OR IN THE INTEGRATION OF PHOTORECEPTOR

METABOLISM.

CC -!- SUBUNIT: Forms a complex with the beta and gamma subunits of

the GTP-binding protein, transducin.

CC -!- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS.

CC -!- MISCELLANEOUS: LIGHT-INDUCED CHANGES IN CYCLIC NUCLEOTIDE LEVELS

MODULATE THE PHOSPHORYLATION OF THIS PROTEIN BY CAMP KINASE.

CC -!- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.

CC -!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS

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CC -----
DR EMBL; M58170; AAA62716.1; -.
DR EMBL; M33529; AAA30349.1; -.
DR PIR; JH0215; JH0215.
DR PIR; A38378; A38378.
DR PIR; A38379; A38379.
DR PDB; 1A0R; 16-FEB-99.
DR InterPro; IPR001200; Phosducin.
DR InterPro; IPR000063; Thiorod.
DR Pfam; PF02114; Phosducin; 1.
DR PRINTS; PR00677; PHOSDUCIN.
KW Vision; Sensory transduction; Phosphorylation; 3D-structure.
FT MOD_RES; 73 73
FT CONFLICT; 44 44 H->P (IN REF. 3).
FT CONFLICT; 238 239 TN->SK (IN REF. 3).
SQ SEQUENCE 245 AA; 28231 MW; 5CA621610401D550 CRC64;

Alignment Scores:
Pred. No.: 87.1 Length: 245
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x PHOS_BOVIN (1-245)

OY 679 TTACTGACGAATTCATATCA 699
DB 197 LeuLeuSerAsnPhelIeser 203

RESULT 16
PHOS_CANFA STANDARD: PRT; 245 AA.
AC 077560;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosducin (PHD) (33 kDa phototransducing protein).
GN PDC.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RX MEDLINE=98382516; PubMed=9714819;
RA Zhang Q., Acland G.M., Parshall C.J., Haskell J., Ray K.,
RA Aguirre G.D.;
RT "Characterization of canine photoreceptor phosducin cDNA and
RT identification of a sequence variant in dogs with photoreceptor
RT dysplasia."
RL Gene 215:231-239(1998).
CC -1- FUNCTION: MAY PARTICIPATE IN THE REGULATION OF VISUAL
CC PHOTOTRANSDUCTION OR IN THE INTEGRATION OF PHOTORECEPTOR
CC METABOLISM.
CC -1- SUBUNIT: Forms a complex with the beta and gamma subunits of
CC the GTP-binding protein, transducin.
CC -1- SUBCELLULAR LOCATION: OUTER AND INNER SEGMENTS OF THE ROD CELLS
CC (BY SIMILARITY).
CC -1- DISEASE: DEFECTS IN PDC ARE THE CAUSE OF PHOTORECEPTOR DYSPLASIA
CC (PD); AN AUTOSOMAL RECESSIVE DISEASE OF MINIATURE SCHNAUZER DOGS
CC CAUSING RETINAL DEGENERATION.
CC -1- SIMILARITY: BELONGS TO THE PHOSDUCIN FAMILY.
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CC -----
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CC -----
DR EMBL; AF046874; AAC27249.1; -.
DR HSSP; P20942; 1B9X.
DR InterPro; IPR001200; Phosducin.
DR InterPro; IPR000063; Thiorod.
DR Pfam; PF02114; Phosducin; 1.
DR PRINTS; PR00677; PHOSDUCIN.
KW Vision; Sensory transduction; Phosphorylation; Disease mutation.
FT MOD_RES; 73 73
FT VARIANT; 82 82 R->G (IN PD).
SQ SEQUENCE 245 AA; 28263 MW; CFA3779E2B7DD236 CRC64;

Alignment Scores:
Pred. No.: 87.1 Length: 245
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x PHOS_CANFA (1-245)

OY 679 TTACTGACGAATTCATATCA 699
DB 197 LeuLeuSerAsnPhelIeser 203

RESULT 17
CHER_BORBU STANDARD: PRT; 283 AA.
ID CHER_BORBU
AC 051069;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase (EC 2.1.1.80).
GN CHER OR BB0040.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RX MEDLINE=98065943; PubMed=9403685;
RC STRAIN=ATCC 35210 / B31;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman C.,
RA Uterback T., Matthey L., McDonald L., Artlach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi."
RL Nature 390:580-586(1997).
CC -1- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC RESIDUES IN MCP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -1- SIMILARITY: CONTAINS 1 CHER-TYPE METHYLTRANSFERASE DOMAIN
CC -----
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 CC -----
 DR EMBL: AF001118; AAC66439.1; -
 DR HSSP: P07801; IBC5.
 DR TIGR: BB0040; -
 DR InterPro: IPR000780; Cher_Metranf.
 DR InterPro: IPR001601; Methyltransf.
 DR InterPro: IPR000051; SAM_bind.
 DR Pfam: PF01739; Cher_1.
 DR Pfam: PF03705; Cher_N_1.
 DR PRINTS: PR00996; CHERMTFRASE.
 DR SMART: SM00138; Metrc; 1.
 DR PROSITE: PS50123; CHER; 1.
 KW Transferrase; Methyltransferase; Chemotaxis; Complete proteome.
 FT DOMAIN 7 283 CHER-TYPE METHYLTRANSFERASE.
 ST SEQUENCE 283 AA; 33560 MW; 2F0E4E9C8BC3EE CRC64;
 Alignment Scores:
 Pred. No.: 84.8 Length: 283
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x CHER_BORBU (1-283)
 QY 266 TTGACATTAACATCAAG 286
 Db 10 LeuasnleasnlethnLys 16
 RESULT 18
 PSTA_RHIL0 STANDARD; PRT; 283 AA.
 ID PSTA_RHIL0
 AC Q98FL4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Phosphate transport system permease protein pstA.
 GN PSTA OR ML13720.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Iidesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -1- FUNCTION: PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR PHOSPHATE; PROBABLY RESPONSIBLE FOR THE TRANSLLOCATION OF THE
 CC SUBSTRATE ACROSS THE MEMBRANE (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
 CC SYSTEM PERMEASE FAMILY. CYSTM SUBFAMILY.
 CC -----
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 CC -----

DR EMBL: AP003002; BAB50553.1; -
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 DR TIGRfams: TIGR00974; 3a0107s02c; 1.
 DR PROSITE: PS00402; BPD_TRANS_P-INN_MEMBR; 1.
 KW Transport; Phosphate transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 20 42 POTENTIAL.
 FT TRANSMEM 70 92 POTENTIAL.
 FT TRANSMEM 105 127 POTENTIAL.
 FT TRANSMEM 137 156 POTENTIAL.
 FT TRANSMEM 188 210 POTENTIAL.
 FT TRANSMEM 254 276 POTENTIAL.
 SQ SEQUENCE 283 AA; 30058 MW; 9CB19047AD82CC7F CRC64;
 Alignment Scores:
 Pred. No.: 84.8 Length: 283
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x PSTA_RHIL0 (1-283)
 QY 532 ACATTGACTGACTTCATTG 552
 Db 263 ThireuthrvalleuAlaleu 269
 RESULT 19
 MRW_BUCAP STANDARD; PRT; 312 AA.
 ID MRW_BUCAP
 AC O85295;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE S-adenosyl-methyltransferase mrw (EC 2.1.1.-).
 GN MRW.
 OS Buchnera aphidicola (subsp. Schizaphis graminum).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=98794;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=98353428; PubMed=9688822;
 RA Thao M.L., Baumann P.;
 RT "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid
 RT endosymbiont) containing the genes dapo-hrrA-llvH-llvH-ftsl-ftsl-
 RT mure.";
 RL Curr. Microbiol. 37:214-216(1998).
 CC -1- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase
 CC activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE MRW FAMILY.
 CC -----
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 CC -----
 CC EMBL: AF060492; AAC32335.1; -
 DR InterPro: IPR002903; Bac_Metnfrse.
 DR Pfam: PF01795; Methyltransf.5; 1.
 DR ProDom: PD004685; Bac_Metnfrse; 1.
 DR TIGRfams: TIGR00006; UPF0117; 1.
 KW Transferrase; Methyltransferase.
 SQ SEQUENCE 312 AA; 36039 MW; F5A7E7F803B31AE7 CRC64;
 Alignment Scores:
 Pred. No.: 83.3 Length: 312
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x MRAW_BUCAPI (1-312)

OY 304 AGAATAGTCAGAACTTCATG 324
|||||
Db 247 Argilevallylsasphenet 253

RESULT 20
REFN_SALTY STANDARD; PRT; 314 AA.
ID REBN_SALTY
AC P26403;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE O antigen biosynthesis rhamnosyltransferase rfbN (EC 2.4.1.-).
GN RFBN OR STM2085.
OS Salmomella typhimurium.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmomella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=91260454; PubMed=1710759;
RA Jiang X.-M., Neal B., Santiago F., Lee S.-J., Romana L.K., Reeves P.R.;
RT "Structure and sequence of the rfb (O antigen) gene cluster of
RT Salmomella serovar typhimurium (strain LT2).";
RL Mol. Microbiol. 5:695-713(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Portnoii L.S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmomella enterica serovar Typhimurium
RT LT2".
RL Nature 413:852-856(2001).
CC -1- CATALYTIC ACTIVITY: CDP-abequose + D-mannosyl-rhamnosyl-D-
CC galactose-1-diphospholipid -> CDP + abequosyl-D-mannosyl-rhamnosyl-
CC -d-galactose-1-diphospholipid.
CC -1- PATHWAY: O ANTIGEN BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.
CC -----
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CC -----
CC EMBL: X56793; CAA40127.1; -
CC EMBL: AE008792; AAL20989.1; -
DR PIR: S15311; S15311.
DR SCyGene: SG10455; rfbN.
DR InterPro: IPR001173; Glycos.transf_2.
DR Pfam: PF00535; Glycos.transf.2; 1.
KW Lipopolysaccharide biosynthesis; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 314 AA; 35508 MW; B15BA176EF2EDB7F CRC64;

Alignment Scores:
Pred. No.: 83.2 Length: 314
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0

DB: 1 Gaps: 0
US-09-817-318-1 (1-780) x REBN_SALTY (1-314)

OY 267 AAGTCATTTGAGAGTAAG 247
|||||
Db 138 LysSerIleVallySerLys 144

RESULT 21
HA10_MOUSE STANDARD; PRT; 328 AA.
ID HA10_MOUSE
AC P14428;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE H-2 class I histocompatibility antigen, K-O alpha chain (H-2K(O))
DE (Fragment).
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85206119; PubMed=3838967;
RA Morita T., Delarbre C., Kress M., Kourilsky P., Gachelin G.;
RT "An H-2K gene of the tw32 mutant at the T/t complex is a close parent
RT of an H-2Kq gene.";
RL Immunogenetics 21:367-383(1985).
CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
CC EMBL: M14827; AAA39656.1; -
CC HSSP: P01901; 2VAA.
DR MCD: MGI:95904; H2-K.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00129; MHC_I; 1.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; Igcl; 1.
DR PROSITE: PS00290; Ig_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 71 EXTRACELLULAR ALPHA-1.
FT DOMAIN 72 163 EXTRACELLULAR ALPHA-2.
FT DOMAIN 164 255 EXTRACELLULAR ALPHA-3.
FT DOMAIN 256 265 CONNECTING PEPTIDE.
FT TRANSMEM 266 289
FT DOMAIN 290 328 CYTOPLASMIC TAIL.
FT DISULFID 82 145 BY SIMILARITY.
FT DISULFID 184 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 328 AA; 36855 MW; ADF1BD811BC37B4 CRC64;

Alignment Scores:
Pred. No.: 82.5 Length: 328
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0

DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x HA1Q_MOUSE (1-328)
 OY 625 ACTTCGATTATTCCTGCCCC 605
 ||||||||||||||||||
 Db 309 ThersaspleserLeupro 315

RESULT 22

HRDD_STRVF STANDARD; PRT: 332 AA.

ID HRDD_STRVF
 AC 060012:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE RNA polymerase principal sigma factor hrdd.
 GN HRDD.

OS Streptomyces viridifaciens.
 OC Bacteria; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_Taxid=48665;
 [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MG456-hf10;
 RA Li W., Parry R.J.;

RT "Nucleotide sequence of the hrdd gene from the valaniycin
 producer, Streptomyces viridifaciens MG456-hf10.";

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
 ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
 THEN IS RELEASED.

-1- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.

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CC EMBL: U60418; AAB03580.1; -
 CC HSSP: P00579; ISIG.

DR InterPro: IPR000943; Sigma_70.
 DR Pfam: PF00140; Sigma70.1.

DR PRINTS: PR00046; SIGMA70CT.
 DR PROSITE: PS00715; SIGMA70.1; 1.

DR PROSITE: PS00716; SIGMA70_2; 1.
 DR Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
 KW DNA-binding.

KM DNA-binding.
 FT DOMAIN 124 137 POLYMERASE CORE BINDING (POTENTIAL).
 FT DNA_BIND 294 313 H-T-H MOTIF (BY SIMILARITY).
 FT SEQUENCE 332 AA; 37099 MW; E21ABC68C57809AE CRC64;

Alignment Scores:

Pred. No.: 82.3 Length: 332
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x HRDD_STRVF (1-332)

OY 459 CACAGAACTGCTTCATTTATA 439
 ||||||||||||||||||

Db 274 GlnArgThrAlaSerIleIle 280

RESULT 23

MDHC_HUMAN

ID MDHC_HUMAN STANDARD; PRT: 333 AA.
 AC P40925;
 DT 01-FEB-1995 (Rel. 31, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Malate dehydrogenase, cytoplasmic (EC 1.1.1.37).
 GN MDH1 OR MDHA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Heart;
 RA Lo A.S.Y., Waye M.M.Y.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RA Lo A.S.Y., Waye M.M.Y.;

RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RA Strausberg R.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE OF 167-180.
 RC TISSUE-Heart;
 RA MEDLINE=95203287; PubMed=7895732;

RL Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;

RT "The human myocardial two-dimensional gel protein database: update
 1994.";

RL Electrophoresis 15:1459-1465(1994).
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.

CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.

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CC EMBL: D55654; BAA09513.1; -
 CC EMBL: U20352; AAC16436.1; -

DR EMBL: BC001484; AA01484.1; -
 DR HSSP: P11708; 4MDH.

DR HSC-2DPAGE: P40925; HUMAN.
 DR Genew: HGNC:6970; MDH1.

DR InterPro: IPR001252; Mdh.
 DR InterPro: IPR001236; Ldh.

DR Pfam: PF00056; Ldh.1.
 DR Pfam: PF02866; Ldh.C.1.

DR PRODOM: PD003052; Mdh.1.
 DR PROSITE: PS00068; Mdh.1.

KW Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT INIT_MET 0
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT BINDING 161 161 PROTON-RELAY.
 FT ACT_SITE 186 186 SUBSTRATE CARBOXYL GROUP.
 FT SEQUENCE 333 AA; 36295 MW; 888F9A/9F6E5E888 CRC64;

Alignment Scores:

Pred. No.: 82.3 Length: 333
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0

DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x MDHC_HUMAN (1-333)

OY 437 GCAAGGAACTCAGACAGAGAA 417
 |||
 Db 316 AlalysglutLeuthrThrglu 322

RESULT 24

MDHC_MOUSE STANDARD: PRT: 333 AA.

ID MDHC_MOUSE
 AC P14152;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Malate dehydrogenase, cytoplasmic (EC 1.1.1.37).
 GN MDH1 OR MOR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=68033094; PubMed=3312200;
 RA Joh T., Takeshima H., Tsuzuki T., Setoyama C., Shimada K.,
 RA Tanase S., Kuramitsu S., Kagamiyama H., Morino Y.;
 RT "Cloning and sequence analysis of cDNAs encoding mammalian cytosolic
 malate dehydrogenase. Comparison of the amino acid sequences of
 RT mammalian and bacterial malate dehydrogenase.";
 RL J. Biol. Chem. 262:15127-15131(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89011964; PubMed=3172222;
 RA Setoyama C., Joh T., Tsuzuki T., Shimada K.;
 RT Structural organization of the mouse cytosolic malate dehydrogenase
 RT gene: comparison with that of the mouse mitochondrial malate
 RT dehydrogenase gene.";
 RL J. Mol. Biol. 202:355-364(1988).
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NADH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUBFAMILY.

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CC EMBL: M29462; AAA39510.1; -;
 DR EMBL: M36084; AAA37423.1; -;
 DR PIR: S02654; DEMSMC.
 DR HSSP: P11708; 4MDH.
 DR SWISS-2DPAGE: P14152; MOUSE.
 DR MGD: MGI:97051; Mor2.
 DR InterPro: IPR001253; Mdh.
 DR InterPro: IPR001236; Ldh.
 DR Pfam: PF00056; Ldh; 1.
 DR Pfam: PF02866; Ldh_C; 1.
 DR ProDom: PD003052; Mdh; 1.
 DR PROSITE: PS00068; MDH; 1.
 KM Oxidoreductase; Tricarboxylic acid cycle; NAD.
 FT INIT_MET 0
 FT ACT_SITE 158 158 PROTON-RELAY.
 FT BINDING 161 161 SUBSTRATE CARBOXYL GROUP.
 FT ACT_SITE 186 186 PROTON-RELAY.
 SO SEQUENCE 333 AA; 36346 MW; 01D5233640ED022A CRC64;

Alignment Scores: 82.3 Length: 333
 Pred. No.:

Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x MDHC_MOUSE (1-333)

OY 437 GCAAGGAACTCAGACAGAGAA 417
 |||
 Db 316 AlalysglutLeuthrThrglu 322

RESULT 25

CX3L_HUMAN STANDARD: PRT: 355 AA.

ID CX3L_HUMAN
 AC P49238;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CX3C chemokine receptor 1 (C-X3-C CMK-1) (CX3CR1) (Fractalkine
 DE receptor) (GPR13) (V28) (Beta chemokine receptor-like 1) (CMK-BRL-1)
 DE (CMKBLR1).
 GN CX3CR1 OR GPR13.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96011651; PubMed=7590284;
 RA Raport C.J., Schweickart V.L., Eddy R.L. Jr., Shows T.B., Gray P.W.;
 RT "The orphan G-protein-coupled receptor-encoding gene V28 is closely
 RT related to genes for chemokine receptors and is expressed in lymphoid
 RT and neural tissues.";
 RL Gene 163:295-299(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95374679; PubMed=7646814;
 RA Combadiere C., Ahuja S.K., Murphy P.M.;
 RT "Cloning, chromosomal localization, and RNA expression of a human
 RT beta chemokine receptor-like gene.";
 RL DNA Cell Biol. 14:673-680(1995).
 RN [3]
 RP CHARACTERIZATION.

RX MEDLINE=98050927; PubMed=9390561;
 RA Imai T., Hieshima K., Haskell C., Baba M., Nagira M., Nishimura M.,
 RA Kakizaki M., Takagi S., Nomiyama H., Schall T.J., Yoshie O.;
 RT "Identification and molecular characterization of fractalkine receptor
 RT CX3CR1, which mediates both leukocyte migration and adhesion.";
 RL Cell 91:521-530(1997).
 RN [4]
 RP CHARACTERIZATION.

RX MEDLINE=98395093; PubMed=9726990.
 RA Combadiere C., Salzwedel K., Smith E.D., Tiffany H.L., Berger E.A.,
 RA Murphy P.M.;
 RT "Identification of CX3CR1, A chemotactic receptor for the human CX3C
 RT chemokine fractalkine and a fusion coreceptor for HIV-1.";
 RL J. Biol. Chem. 273:23799-23804(1998).
 RN [5]
 RP VARIANTS ALA-57; ILE-122; ILE-249 AND MET-280.

RX MEDLINE=20196025; PubMed=10731151;
 RA Faure S., Meyer L., Costagliola D., Vaneensbergh C., Genin E.,
 RA Autran B., Delfraissy J.-F., McDermott D.H., Murphy P.M., Debre P.,
 RA Theodorou I., Combadiere C.;
 RT "Rapid progression to AIDS in HIV+ individuals with a structural
 RT variant of the chemokine receptor CX3CR1.";
 RL Science 287:2274-2277(2000).
 CC -1- FUNCTION: RECEPTOR FOR THE CX3C CHEMOKINE FRACTALKINE AND MEDIATES
 CC BOTH ITS ADHESIVE AND MIGRATORY FUNCTIONS. ACTS AS CO-RECEPTOR
 CC WITH CD4 FOR HIV-1 VIRUS ENVELOPE PROTEIN (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LYMPHOID AND NEURAL TISSUES.
 CC -1- DISEASE: INCREASED SUSCEPTIBILITY TO HIV INFECTION AND RAPID

PROGRESSION TO AIDS ARE ASSOCIATED WITH THE I-249/N-280 HAPLOTYPE.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: U20350; AAA91783.1; -
 CC EMBL: U28934; AAA87032.1; -
 CC Genew: HGNC:2558; CX3CRL.
 CC MIM: 601470; -
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOOPS.
 CC PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 CC PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 CC G-protein coupled receptor; Transmembrane; Polymorphism.
 FT DOMAIN 1 31
 FT TRANSMEM 32 59
 FT DOMAIN 60 69
 FT TRANSMEM 70 90
 FT DOMAIN 91 103
 FT TRANSMEM 104 125
 FT DOMAIN 126 142
 FT TRANSMEM 143 167
 FT DOMAIN 168 195
 FT TRANSMEM 196 215
 FT DOMAIN 216 231
 FT TRANSMEM 232 256
 FT DOMAIN 257 273
 FT TRANSMEM 274 297
 FT DOMAIN 298 355
 FT DISULFID 102 175
 FT VARIANT 57 57
 FT VARIANT 122 122
 FT VARIANT 249 249
 FT VARIANT 280 280
 FT SEQUENCE 355 AA; 40396 MW; C59DC5F4C4312F22 CRC64;
 Alignment Scores:
 Pred. No.: 81.3 Length: 355
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x C3X1_HUMAN (1-355)
 QY 704 TTAATTCCTCGTGTCTATA 724
 Db 232 LeuILEuLeuValIle 238
 RESULT 26
 HAID_MOUSE STRAND: PRT; 368 AA.
 ID HAID_MOUSE
 AC P01902;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 21-JUL-1986 (rel. 01, Last sequence update)
 DT 15-JUL-1999 (rel. 38, Last annotation update)
 DE H-2 class I histocompatibility antigen, K-D alpha chain precursor
 DE (H-2K(D)).
 GN H2-K.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kvist S., Roberts L., Dobberstein B.;
 RT "Mouse histocompatibility genes: structure and organisation of a Kd
 RT gene.";
 RL EMBO J. 2:245-254(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=83143367; PubMed=6298749;
 RA Lalanne J.-L., Delarbre C., Gachet G., Kourilsky P.;
 RT "A cDNA clone containing the entire coding sequence of a mouse H-2Kd
 RT histocompatibility antigen.";
 RL Nucleic Acids Res. 11:1567-1577(1983).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NOD/LT;
 RA Girgis K.R., Capra D.J., Stroyanowski I.;
 RP Submitted (Mar-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c;
 RX MEDLINE=99086740; PubMed=9869916;
 RA Wang M., Stepkowski S.M., Hebert J.S., Tian L., Yu J., Kahan B.D.;
 RT "Nucleotide sequences of three H-2K and three H-2D complementary DNA
 RT clones coding mouse class I MHC heavy chain proteins.";
 RL Ann. Transplant. 1:26-31(1996).
 RN [5]
 RP SEQUENCE OF 22-119.
 RX MEDLINE=81232882; PubMed=7018573;
 RA Kimball E.S., Matheson S.G., Coligan J.E.;
 RT "Amino acid sequence of residues 1-98 of the K-2kb murine major
 RT histocompatibility alloantigen: comparison with H-2kb and H-2db
 RT reveals extensive localized differences.";
 RL Biochemistry 20:3301-3308(1981).
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 CC THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN).
 CC
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 CC
 CC EMBL: J00402; AAA39652.1; -
 CC EMBL: U36065; AAA89205.1; -
 CC EMBL: U47329; AAB17607.1; -
 CC PIR: A02204; HLMKRD.
 CC HSP: P01899; 1B29.
 CC MGD: MGI:95904; H2-K.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003597; Ig_c1.
 CC InterPro: IPR01039; MHC_I.
 CC Pfam: PF00047; Ig_1.
 CC Pfam: PF00129; MHC_I_1.
 CC Prodom: P000050; MHC_I_1.
 CC SMART: SM00407; Ig_c1_1.
 CC PROSITE: PS00290; Ig_MHC; 1.
 CC MHC I; Transmembrane; Glycoprotein; Signal.
 FT CHAIN 1 21
 FT SIGNAL 22 368
 FT DOMAIN 22 111
 FT DOMAIN 112 203
 FT DOMAIN 204 295
 FT H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
 FT K-D ALPHA CHAIN.
 FT EXTRACELLULAR ALPHA-1.
 FT EXTRACELLULAR ALPHA-2.
 FT EXTRACELLULAR ALPHA-3.

```
FT DOMAIN 296 305 CONNECTING PEPTIDE.
FT TRANSMEM 306 328
FT DOMAIN 329 368 CYTOPLASMIC TAIL.
FT DISULFID 122 185 BY SIMILARITY.
FT DISULFID 224 280 BY SIMILARITY.
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 135 135 Q -> H (IN REF. 2).
SQ SEQUENCE 368 AA: 41490 MW: 4C83897C8CF76E5 CRC64;

Alignment Scores:
Pred. No.: 80.8 Length: 368
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x HAIW_MOUSE (1-368)
QY 625 ACTTCGATTATCCCTGCC 605
DB 349 ThrSerAspLeuSerLeuPro 355

RESULT 27
HAIW_MOUSE
ID HAIW_MOUSE STANDARD: PRT: 368 AA.
AC P03951: P03950;
DT 23-OCT-1986 (rel. 02, Created)
DT 01-JAN-1990 (rel. 13, Last sequence update)
DT 01-FEB-1996 (rel. 33, Last annotation update)
DE H-2 class I histocompatibility antigen, K-W28 alpha chain precursor.
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85206119; PubMed=3838967;
RA Morita T., Delafre C., Kress M., Kourilsky P., Gachelin G.;
RT "An H-2K gene of the tw32 mutant at the T/t complex is a close parent
RT of an H-2Kq gene."
RL Immunogenetics 21:367-383(1985).
RN [2]
RP SEQUENCE OF 258-368 FROM N.A.
RC STRAIN=SMR;
RX MEDLINE=84068207; PubMed=6689056;
RA Kress M., Glaros D., Khoury G., Jay G.;
RT "Alternative RNA splicing in expression of the H-2K gene.";
RL Nature 306:602-604(1983).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
CC THE IMMUNE SYSTEM.
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN).
CC -----
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CC -----
DR EMBL: M14825; AAA3657.1; -
DR EMBL: X00172; CAA2497.1; -
DR PIR: A02197; A02197.
DR PIR: A02196; A02196.
DR HSSP: P01901; 2VAA.
DR MGD: MGI:95904; H2-K.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
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DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00129; MHC_T; 1.
DR ProDom: PD000050; MHC_I; 1.
DR SMART: SM00407; IG1; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW MHC I; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 21
FT CHAIN 22 368
FT FT
FT DOMAIN 22 111 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT DOMAIN 112 203 K-W28 ALPHA CHAIN.
FT DOMAIN 204 295 EXTRACELLULAR ALPHA-1.
FT DOMAIN 296 305 EXTRACELLULAR ALPHA-2.
FT TRANSMEM 306 329 EXTRACELLULAR ALPHA-3.
FT TRANSMEM 306 329 CONNECTING PEPTIDE.
FT DOMAIN 330 368 CYTOPLASMIC TAIL.
FT DISULFID 122 185 BY SIMILARITY.
FT DISULFID 107 107 BY SIMILARITY.
FT CARBOHYD 197 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 368 AA: 41103 MW: C07A9CDA458BA58F CRC64;

Alignment Scores:
Pred. No.: 80.8 Length: 368
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x HAIW_MOUSE (1-368)
QY 625 ACTTCGATTATCCCTGCC 605
DB 349 ThrSerAspLeuSerLeuPro 355

RESULT 28
HAIW_MOUSE
ID HAIW_MOUSE STANDARD: PRT: 369 AA.
AC P01901;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE H-2 class I histocompatibility antigen, K-B alpha chain precursor
DE (H-2K(b)).
GN H2-K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Weiss E., Golden L., Zakut R., Mellor A., Fahrner K., Kvist S.,
RA Flavell R.A.;
RT "The DNA sequence of the H-2K(b) gene: evidence for gene conversion
RT as a mechanism for the generation of polymorphism in
RT histocompatibility antigens."
RL EMBO J. 2:453-462(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/10;
RX MEDLINE=99086740; PubMed=9869916;
RA Wang M., Stepkowski S.M., Hebert J.S., Tian L., Yu J., Kahan B.D.;
RT "Nucleotide sequences of three H-2K and three H-2D complementary DNA
RT clones coding mouse class I MHC heavy chain proteins."
RL Ann. Transplant. 1:26-31(1996).
RN [3]
RP SEQUENCE OF 87-369 FROM N.A.
RX MEDLINE=82247837; PubMed=6954478;
RA Reyes A.A., Schold M., Itakura K., Wallace R.B.;
RT "Isolation of a cDNA clone for the murine transplantation antigen
RT H-2k."
RL Proc. Natl. Acad. Sci. U.S.A. 79:3270-3274(1982).
```

[4]
 RN SEQUENCE OF 22-367.
 RP MEDLINE=82068960; Pubmed=7306483;
 RA Uehara H., Coligan J.E., Nathenson S.G.;
 RT "Amino acid sequence of the carboxyl-terminal hydrophilic region of
 the H-2Kb MHC alloantigen. Completion of the entire primary structure
 of the H-2Kb molecule.";
 RL Biochemistry 20:5940-5945(1981).
 (5)
 RN REVISIONS TO 284; 296 AND 297.
 RP MEDLINE=82247837; Pubmed=6954478;
 RA Coligan J.;
 RT Unpublished results, cited by:
 RL Reyes A.A., Schold M., Itakura K., Wallace R.B.;
 RL Proc. Natl. Acad. Sci. U.S.A. 79:3270-3274(1982).
 (6)
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 22-295.
 RP MEDLINE=92367003; Pubmed=1323877;
 RA Fremont D.H., Matsumura M., Stura E.A., Peterson P.A., Wilson I.A.;
 RT "Crystal structures of two viral peptides in complex with murine MHC
 class I H-2Kb.";
 RL Science 257:919-927(1992).
 (7)
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 22-295 IN COMPLEX WITH CD8A.
 RP MEDLINE=99021475; Pubmed=9806638;
 RA Kern P.S., Teng M.K., Smolyar A., Liu J.H., Liu J., Hussey R.E.,
 RA Spoerl R., Chang H.-C., Reinherz E.L., Wang J.-H.;
 RT "Structural basis of CD8 coreceptor function revealed by
 crystallographic analysis of a murine CD8alpha alpha ectodomain
 fragment in complex with H-2Kb.";
 RL Immunity 9:519-530(1998).
 (8)
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-295.
 RP MEDLINE=99146375; Pubmed=10023770;
 RA Speir J.A., Abdel-Motal U.M., Jondal M., Wilson I.A.;
 RT "Crystal structure of an MHC class I presented glycopeptide that
 generates carbohydrate-specific CTL.";
 RL Immunity 10:51-61(1999).
 (9)
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
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 CC
 DR EMBL: J00400; AAA39648.1; -;
 DR EMBL: U47328; AAB17606.1; -;
 DR EMBL: V00746; CAA24119.2; -;
 DR EMBL: V00747; CAA24119.2; JOINED.
 DR PIR: A02202; HLMSKB.
 DR PDB: 2VAA; 20-JUN-96.
 DR PDB: 2VAB; 20-JUN-96.
 DR PDB: 2CKB; 09-SEP-98.
 DR PDB: 1BOH; 19-AUG-98.
 DR PDB: 1KEG; 09-FEB-99.
 DR MGD: MGI:95904; H2-K.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; Ig; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SM00407; IGc1; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KM MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
 FT SIGNAL 1 21
 FT CHAIN 22 369 H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN,

FT DOMAIN 22 111 K-B ALPHA CHAIN.
 FT DOMAIN 112 203 EXTRACELLULAR ALPHA-1.
 FT DOMAIN 204 295 EXTRACELLULAR ALPHA-2.
 FT DOMAIN 296 305 EXTRACELLULAR ALPHA-3.
 FT TRANSMEM 306 328 CONNECTING PEPTIDE.
 FT DOMAIN 329 369 CYTOPLASMIC TAIL.
 FT DISULFID 122 185
 FT CARBOHYD 107 107
 FT CARBOHYD 197 197
 FT CONFLICT 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 334 334 E -> Q (IN REF. 4).
 FT CONFLICT 364 364 N -> A (IN REF. 4).
 FT CONFLICT 364 364 D -> P (IN REF. 4).
 SO SEQUENCE 369 AA; 41302 MW; 3D2F125318193443 CRC64;
 Alignment Scores:
 Pred. No.: 80.8 Length: 369
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x HA1B_MOUSE (1-369)
 QY 625 ACTTCGTGATTATCCGCCCC 605
 DB 350 ThrsraspleuSerLeupro 356
 RESULT 29
 HA1K_MOUSE
 ID HA1K_MOUSE STANDARD: PRT: 369 AA.
 AC P04223;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE H-2 class I histocompatibility antigen, K-K alpha chain precursor
 DE (H-2K(K)).
 GN H2-K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087950; Pubmed=6096831;
 RA Arnold B., Burgert H.-G., Archibald A.L., Kvist S.;
 RT "Complete nucleotide sequence of the murine H-2Kk gene. Comparison of
 three H-2K locus alleles.";
 RL Nucleic Acids Res. 12:9473-9487(1984).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RX MEDLINE=88060499; Pubmed=3680952;
 RA Watts S., Vogel J.M., Harriman W.D., Itoh T., Stauss H.J.,
 RA Goodenow R.S.;
 RT "DNA sequence analysis of the C3H H-2K and H-2D loci. Evolutionary
 relationships to H-2 genes from four other mouse strains.";
 RL J. Immunol. 139:3878-3885(1987).
 (3)
 CC -1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
 THE IMMUNE SYSTEM.
 CC -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 MICROGLOBULIN).
 CC
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 CC

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Flischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervlov G., Milshina N.V., Modyarty C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang M., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RA Science 287:2185-2195(2000).
 RL [3]
 RN REVISIONS.
 RC STRAIN-Berkeley;
 RA Misra S., Crosby M.A., Mathews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochank S.E., Smith C.D.,
 RA Tupy J.E., Bergman C.M., Berman B.P., Carlson J.W., Gelinger S.E.,
 RA Clapp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,
 RA Harris N.L., Krommiller B., Marshall B., Millburn G.H., Richter J.,
 RA Russo S., Searle S.M.J., Smith E., Shu S., Smutnick F.,
 RA Whitfield E.J., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Mungall C.J., Lewis S.E.;
 RA "Annotation of *Drosophila melanogaster* genome.";
 RA Submitted (MAY-2002) to the EMBL/Genbank/DBU databases.
 RL [4]
 RN IDENTIFICATION AND TISSUE SPECIFICITY.
 RP MEDLINE-99166868; PubMed-10069338;
 RX Clyne P.J., Marr C.G., Freeman M.R., Lessing D., Kim J., Carlson J.R.;
 RA "A novel family of divergent seven-transmembrane proteins: candidate
 RT odorant receptors in *Drosophila*.";
 RL Neuron 22:327-338(1999).
 CC -i- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
 CC RECEPTOR.
 CC -i- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -i- TISSUE SPECIFICITY: EXPRESSED IN A SUBSET OF 17 OLFACTORY RECEPTOR
 CC NEURONS IN THE MAXILLARY PALP.
 CC -i- SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
 CC RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: AE003830; AAF58634.2; -;
 DR FlyBase: FBgn0026388; OF46a.
 DR InterPro: IPR004117; 7tm_6.
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF02949; 7tm_6; 1.
 KW Transmembrane; G-protein coupled receptor; Olfaction; Glycoprotein;
 KW Multigene family.
 FT DOMAIN 1 37 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 38 58 1 (POTENTIAL).
 FT DOMAIN 59 65 2 (POTENTIAL).
 FT TRANSMEM 66 86 3 (POTENTIAL).
 FT DOMAIN 87 127 4 (POTENTIAL).
 FT TRANSMEM 128 148 5 (POTENTIAL).
 FT DOMAIN 149 170 6 (POTENTIAL).
 FT TRANSMEM 171 191 7 (POTENTIAL).
 FT DOMAIN 192 255 8 (POTENTIAL).
 FT TRANSMEM 256 276 9 (POTENTIAL).
 FT DOMAIN 277 287 10 (POTENTIAL).
 FT TRANSMEM 288 308 11 (POTENTIAL).
 FT DOMAIN 309 354 12 (POTENTIAL).
 FT TRANSMEM 355 375 13 (POTENTIAL).
 FT DOMAIN 376 385 14 (POTENTIAL).
 SQ SEQUENCE 385 AA; 44463 MW; BB062862B7A59310 CRC64;
 Alignment Scores:
 Pred. No.: 80.1 Length: 385
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 1 Gaps: 0
 US-09-817-318-1 (1-780) x 046A_DROME (1-385)
 QY 415 TTTTCTCTGTCGAGTTCCTTT 435
 Db 362 PheSerValSerPhe 368
 |||||
 RESULT 32
 Y360_MYCGE
 ID Y360_MYCGE STANDARD; PRT; 411 AA.
 AC 049426;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Hypothetical protein MG360.
 GN MG360.
 OS Mycoplasma genitalium.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxId=2097;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 33530 / G-37;
 RX MEDLINE-96026346; PubMed-7569993;
 RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
 RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
 RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
 RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
 RA Tomb J.-F., Dougherty B.A., Bolt K.F., Hu P.-C., Lucier T.S.,
 RA Peterson S.N., Smith H.O., Hutchison C.A. II, Venter J.C.;
 RA "The minimal gene complement of *Mycoplasma genitalium*.";
 RL Science 270:397-403(1995).
 CC -i- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
 CC -----
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 CC -----
 DR EMBL: U39717; AAC71585.1; -;
 DR TIGR: MG360; -;
 DR InterPro: IPR001126; UMOC_1like.
 DR Pfam: PF00817; IMS; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 411 AA; 47466 MW; F3FA0C41E9018BAD CRC64;
 Alignment Scores:
 Pred. No.: 79.2 Length: 411

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Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x Y360_MYCGE (1-411)

OY 622 AACGTACTGCAATACAAAG 642
DB 326 Lysleuenserletnrltlys 332

RESULT 33
AMSI_ERWAM STANDARD: PRT: 415 AA.
ID AMSI_ERWAM
AC Q46637;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Amylovoran biosynthesis protein amsv.
GN AMSJ.
OS Erwinia amylovora.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
OX NCBI_TaxID=552;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95319333; PubMed=7596293;
RA Bugert P., Gelder K.;
RT "Molecular analysis of the amv operon required for exopolysaccharide
RT synthesis of Erwinia amylovora.";
RL MOL. Microbiol. 15:917-933(1995).
CC -1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF AMYLOVORAN WHICH
CC FUNCTIONS AS A VIRULENCE FACTOR.
CC -1- PATHWAY: Exopolysaccharide biosynthesis.
CC -1- SIMILARITY: TO E.COLI COLANIC ACID BIOSYNTHESIS PROTEIN WCAR.
CC
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CC
CC -----
CC DR EMBL: X77921; CAA54888.1; -
CC KM Exopolysaccharide synthetis.
CC SQ SEQUENCE 415 AA; 46397 MW; 6295D941C55BD2BD CRC64;

Alignment Scores:
Pred. No.: 79 length: 415
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x AMSI_ERWAM (1-415)

OY 77 GCTGTAGCTATAATTATGAG 97
DB 341 AlavalaileasntyrGlu 347

RESULT 34
POTE_HAEIN STANDARD: PRT: 435 AA.
ID POTE_HAEIN
AC P44768;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putrescine-ornithine antiporter (Putrescine transport protein).
GN POTE OR H10590.
OS Haemophilus influenzae.

```

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OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Rd / KM20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Ueberback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: PROBABLE PUTRESCINE-ORNITHINE ANTIPORTER
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMEASES.
CC
CC -----
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CC
CC -----
CC DR EMBL: U32740; AAC22247.1; -
CC DR TIGR: H10590; -
CC DR InterPro: IPR002293; AA/rel.prmaseel.
CC DR InterPro: IPR004841; Permease.
CC DR InterPro: IPR004754; R/O-antiport.
CC DR Pfam: PF00324; aa-permeases; 1.
CC DR TIGRFAMs: TIGR00905; 2A0302; 1.
CC KW Transport; Antiport; Amino-acid transport; Transmembrane;
CC KW Inner membrane; Complete proteome.
CC FT TRANSMEM 8 POTENTIAL.
CC FT TRANSMEM 39 59 POTENTIAL.
CC FT TRANSMEM 95 115 POTENTIAL.
CC FT TRANSMEM 117 137 POTENTIAL.
CC FT TRANSMEM 148 168 POTENTIAL.
CC FT TRANSMEM 185 205 POTENTIAL.
CC FT TRANSMEM 224 244 POTENTIAL.
CC FT TRANSMEM 275 295 POTENTIAL.
CC FT TRANSMEM 320 340 POTENTIAL.
CC FT TRANSMEM 354 374 POTENTIAL.
CC FT TRANSMEM 386 406 POTENTIAL.
CC FT TRANSMEM 409 429 POTENTIAL.
CC SQ SEQUENCE 435 AA; 46348 MW; C4D992217975B5A8 CRC64;

Alignment Scores:
Pred. No.: 78.3 length: 435
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x POTE_HAEIN (1-435)

OY 233 ACAGCTTAGACGACCTTACTC 253
DB 329 Thralaengintnrlleu 335

RESULT 35
G6PI_LACIA

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ID G6PI_LACLA STANDARD: PRT: 447 AA.
AC P81181;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (Phosphoglucose
isomerase) (PGI) (Phosphohexose isomerase) (PHI).
GN PGI OR PGI OR L2168.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria: Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Mincker P., Manger S., Jallion O., Malarne K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
RT Genome Res. 11:731-753(2001).
RL [2]
RN SEQUENCE OF 1-19.
RX MEDLINE=97312580; PubMed=9169021;
RA Nomura M., Nakajima I., Matsuzaki M., Kimoto H., Suzuki I., Aso H.;
RT "The N-terminal sequence of Lactococcus lactis phosphoglucose
isomerase purified by affinity chromatography differs from the other
species.";
RT Arch. Biochem. Biophys. 341:315-320(1997).
RL -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-
phosphate.
CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.
CC -----
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CC -----
DR EMBL: AE006445; AAK06266.1; -
DR HSSP: P13376; 2PGI.
DR InterPro: IPR001672; G6P_Isomerase.
DR Pfam: PF00342; PGI.1.
DR PRINTS: PR00662; G6PISOMERASE.
DR PROSITE: PS00765; P_GLUCOSE_ISOMERASE_1; 1.
DR PROSITE: PS00174; P_GLUCOSE_ISOMERASE_2; 1.
KW Isomerase; Gluconeogenesis; Glycolysis; Complete proteome.
FT INIT_MET 0
FT ACT_SITE 310 BY SIMILARITY.
FT ACT_SITE 424 BY SIMILARITY.
FT ACT_SITE 424
SQ SEQUENCE 447 AA; 49463 MW; 40DD4FC7D106FD29 CRC64;

Alignment Scores:
Pred. No.: 78 Length: 447
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x G6PI_LACLA (1-447)

QY 391 TTATCCACTGTTTGTAAAC 411
DB 94 LeuSerAsnSerPheValasn 100

RESULT 36
YKRB_YEAST STANDARD: PRT: 453 AA.
AC P34252;
RN [2]

DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Hypothetical 52.3 kDa protein in HAP4-ARI intergenic region.
GN YK108W OR YK1463.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=94152173; PubMed=8109175;
RA Cheret G., Pallier C., Valens M., Dajman-Fornier B., Fukuhara H.,
RA Bolotin-Fukuhara M., Sor F.;
RT "The DNA sequence analysis of the HAP4-LAP4 region on chromosome XI
of Saccharomyces cerevisiae suggests the presence of a second
RT aspartate aminotransferase gene in yeast.";
RT Yeast 9:1259-1265(1993).
RL [2]
RN SEQUENCE OF 1-19.
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CC -----
DR EMBL: X71133; CAA50449.1; -
DR EMBL: Z28108; CAA81948.1; -
DR PIR: S37935; S37935.
DR PIR: S39096; S39096.
DR SCD: S0001591; YK1108W.
KW Hypothetical protein.
SQ SEQUENCE 453 AA; 52271 MW; 52B2969C97AAENC8 CRC64;

Alignment Scores:
Pred. No.: 77.8 Length: 453
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x YKRB_YEAST (1-453)

QY 679 ATGAATTTATCACTATAAA 659
DB 97 MetAsnLeuSerProIleIys 103

RESULT 37
NU4M_HUMAN STANDARD: PRT: 459 AA.
AC P03905;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN MTND4 OR ND4.
OS Homo sapiens (Human).
OG Mitochondrion.
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=81173052; PubMed=7219534;
RA Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.,
RA Coulson A.R., Drouin J., Eperon I.C., Nierlich D.P., Roe B.A.,
RA Sanger F., Schreier P.H., Smith A.J.H., Staden R., Young I.G.;
RT "Sequence and organization of the human mitochondrial genome.";
RT Nature 290:457-465(1981).
RL [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=92315217; PubMed=1377597;
RA Lu X., Walker T., Macmanus J.P., Seligy V.L.;
RT "Differentiation of H7-29 human colonic adenocarcinoma cells
RT correlates with increased expression of mitochondrial RNA: effects of
RT trehalose on cell growth and maturation.";
RL Cancer Res. 52:3718-3725(1992).
RN [3]
RP SEQUENCE OF 308-459 FROM N.A.
RX MEDLINE=82242101; PubMed=6284948;
RA Brown W.M., Prager E.M., Wang A., Wilson A.C.;
RT "Mitochondrial DNA sequences of primates: tempo and mode of
RT evolution.";
RL J. Mol. Evol. 18:225-239(1982).
RN [4]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=85188293; PubMed=3921850;
RA Chomay A., Mariottini P., Cleeter M.W.J., Ragan C.I., Matsuno-Yagi A.
RT "Six unidentified reading frames of human mitochondrial DNA encode
RT components of the respiratory-chain NADH dehydrogenase.";
RL Nature 314:592-597(1985).
RN [5]
RP VARIANT LHON HIS-340.
RX MEDLINE=89072713; PubMed=3201231;
RA Wallace D.C., Singh G., Lott M.T., Hodge J.A., Schurr T.G.,
RA Lezza A.M., Elsas L.J. II, Nikoskelainen E.K.;
RT "Mitochondrial DNA mutation associated with Leber's hereditary optic
RT neuropathy.";
RL Science 242:1427-1430(1988).
RN [6]
RP CHARACTERIZATION OF VARIANT LHON HIS-340.
RX MEDLINE=92070510; PubMed=1959619;
RA Mäkelä A., Huoponen K., Savontaus M.-L., Nikoskelainen E.,
RA Wikström M.;
RT "Electron transfer properties of NADH:ubiquinone reductase in the
RT ND1/3460 and the ND4/11778 mutations of the Leber hereditary optic
RT neuroretinopathy (LHON).";
RL FEBS Lett. 292:289-292(1991).
RN [7]
RP VARIANT LHON HIS-340.
RX MEDLINE=92070953; PubMed=1959931;
RA Korman B.A., Schuster H., Berringer T.A., Leo-Kottler B.;
RT "Detection of the G to A mitochondrial DNA mutation at position 11778
RT in German families with Leber's hereditary optic neuropathy.";
RL Hum. Genet. 88:98-100(1991).
RN [8]
RP VARIANTS PRO-79; PRO-109; THR-132 AND THR-294.
RX MEDLINE=92098084; PubMed=1757091;
RA Marzuki S., Noer A.S., Lertit P., Thyagarajan D., Kapsa R.,
RA Uthmanapoli P., Byrne E.;
RT "Normal variants of human mitochondrial DNA and translation products:
RT the building of a reference data base.";
RL Hum. Genet. 88:139-145(1991).
RN [9]
RP VARIANT MELAS ALA-109.
RX MEDLINE=92359093; PubMed=1323207;
RA Lertit P., Noer A.S., Jean-Francois M.J.B., Kapsa R., Dennett X.,
RA Thyagarajan D., Lethlean K., Byrne E., Marzuki S.;
RT "A new disease-related mutation for mitochondrial encephalopathy
RT lactic acidosis and stroke-like episodes (MELAS) syndrome affects the
RT ND4 subunit of the respiratory complex I.";
RL Am. J. Hum. Genet. 51:457-468(1992).
RN [10]
RP VARIANT LDYT ILE-313.
RX MEDLINE=96220221; PubMed=8644732;
RA De Vries D.D., Went L.N., Bruyn G.W., Scholte H.R., Hofstra R.M.W.,
RA Bolhuis P.A., van Oost B.A.;
RT "Genetic and biochemical impairment of mitochondrial complex I
RT activity in a family with Leber hereditary optic neuropathy and
RT hereditary spastic dystonia.";
RL Am. J. Hum. Genet. 58:703-711(1996).
RN [11]

RP	VARIANT:	LHON HIS-340.
RX	MEDLINE:	968112486; PubMed=9452107.
RA	Sudoyo H.,	Stjepan M., Malik S., Poesponegoro H.D., Marzuki S.;
RT	"Leber's hereditary optic neuropathy in Indonesia: two families with	
RT	the mtDNA 11778G>A and 14484T>C mutations."	
RL	Hum. Mutat. Suppl. 1:S271-S274(1998).	
-I-	CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.	
CC	-I- DISEASE: DEFECTS IN MTND4 ARE ONE OF THE CAUSES OF LEBER'S	
CC	HEREDITARY OPTIC NEUROPATHY (LHON), A MATERIALLY INHERITED DISEASE	
CC	RESULTING IN ACUTE BILATERAL BLINDNESS DUE TO RETINAL DEGENERATION	
CC	PREDOMINANTLY IN YOUNG MEN. CARDIAC CONDUCTION DEFECTS AND	
CC	PERIOLOCAL DEFECTS HAVE ALSO BEEN DESCRIBED. RESULTING IN OPTIC	
CC	NERVE DEGENERATION AND CARDIAC DYSRHYTHMIA.	
CC	-I- DISEASE: IN SOME PATIENTS, LHON IS ASSOCIATED WITH DYSTONIA AND	
CC	IS KNOWN AS 'LDYT'.	
CC	-I- DISEASE: DEFECTS IN MTND4 ARE ONE OF THE CAUSES OF MELAS SYNDROME;	
CC	A DISEASE CHARACTERIZED BY MITOCHONDRIAL ENCEPHALOPATHY, LACTIC	
CC	ACIDOSIS, AND STROKE-LIKE EPISODES.	

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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
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CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch)	

DR	EMBL; J01415; AAB56952.1; -;	
DR	EMBL; V00662; CAA24035.1; -;	
DR	PIR; A00434; DNHUN4.	
DR	GeneW; HGNC:7459; MTND4.	
DR	MIM; 516003; -;	
DR	MIM; 535000; -;	
DR	MIM; 540000; -;	
DR	InterPro; IPR003918; NADhub_oxrred4.	
DR	InterPro; IPR001750; Oxidored_q1.	
DR	InterPro; IPR000260; Oxidored_q5_N.	
DR	Pfam; PF00361; Oxidored_q1; 1.	
DR	Pfam; PF01059; Oxidored_q5_N; 1.	
DR	PRINTS; PR01437; NDOXDPTASE4.	
KW	Oxidoreductase; NAD; Ubiquinone; Mitochondion; Polymorphism;	
KW	Leber's hereditary optic neuropathy; Disease mutation.	
FT	VARIANT	79
FT		/FtId-VAR_008599.
FT	VARIANT	109
FT		/FtId-VAR_008600.
FT	VARIANT	109
FT		T->A (IN MELAS).
FT	VARIANT	132
FT		/FtId-VAR_004759.
FT	VARIANT	132
FT		I->T.
FT	VARIANT	294
FT		/FtId-VAR_008601.
FT	VARIANT	313
FT		M->T.
FT	VARIANT	340
FT		/FtId-VAR_008602.
FT	VARIANT	340
FT		V->I (IN LDYT; POSSIBLE RARE PRIMARY MUTATION).
FT	VARIANT	340
FT		/FtId-VAR_008393.
FT	VARIANT	340
FT		R->H (IN LHON; PRIMARY MUTATION; ALMOST NO VISION RECOVERY; MOST FREQUENT MUTATION; SEEMS TO HAVE NO EFFECT ON ELECTRON TRANSFER ACTIVITY OF THE COMPLEX IN INNER MITOCHONDRIAL MEMBRANE PREPARATIONS).
FT	VARIANT	340
FT		/FtId-VAR_004760.
FT	VARIANT	340
FT		/FtId-VAR_004760.
SO	SEQUENCE	459 AA; 51580 MW; 2BE5B81FBBD270AF CMC64;
Alignment Scores:		
Pred. No.:	77.6	Length: 459
Score:	7.00	Matches: 7
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	2.92%	Indels: 0
DB:	1	Gaps: 0

```

US-09-817-318-1 (1-780) x NU4M_HUMAN (1-459)
Oy 649 AACATACTTTGTTATTGACA 629
    |||||||
Db 390 AsnIleThrLeuLeuThr 396

RESULT 38
NU4M_BRARE
ID NU4M_BRARE STANDARD; PRT; 460 AA.
AC P31394;
DT 01-JUL-1993 (rel. 26, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN NMDA OR ND4.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OX Cyprinidae; Danio.
RN NCBITaxID=7955;
RP SEQUENCE FROM N.A.
RX STRAIN=AB:
RX MEDLINE=21549095; PubMed=11691861;
RA Broughton R.E., Milam J.E., Roe B.A.;
RT "The complete sequence of the zebrafish (Danio rerio) mitochondrial
RT genome and evolutionary patterns in vertebrate mitochondrial DNA.";
RL Genome Res. 11:1958-1967(2001).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AC024175; AAF74306.1; -
DR ZFIN: ZDB-GENE-011205-10; mtn4.
DR InterPro: IPR001750; Oxidored_q1.
DR InterPro: IPR000260; Oxidored_q5_N.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF01059; oxidored_q5_N; 1.
DR KX Oxidoreductase; NAD; ubiquinone; Mitochondrion.
DR KW Oxidoreductase; NAD; ubiquinone; Mitochondrion.
SQ SEQUENCE 460 AA; 51529 MW; 1615202B56513143 CRC64;

Alignment Scores:
Pred. No.: 77.5 Length: 460
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
De: 1 Gaps: 0

US-09-817-318-1 (1-780) x NU4M_BRARE (1-460)
Oy 273 TTACATCACAAGAGGTC 293
    |||||||
Db 413 LeuThrSerGlnArgLysSer 419

RESULT 39
PRTC_RAT
ID PRTC_RAT STANDARD; PRT; 461 AA.
AC P31394;
DT 01-JUL-1993 (rel. 26, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Vitamin-K dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysin IIA) (Anticoagulant protein C) (Blood coagulation
DE factor XIV).
GN PROC.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBITaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=92329550; PubMed=1627650;
RA Okafuji T., Maekawa K., Nawa K., Marumoto Y.;
RT "The cDNA cloning and mRNA expression of rat protein C.";
RL Biochim. Biophys. Acta 1131:329-332(1992).
CC -1- FUNCTION: PROTEIN C IS A VITAMIN K-DEPENDENT SERINE PROTEASE THAT
CC REGULATES BLOOD COAGULATION BY INACTIVATING FACTORS VA AND VILLA
CC IN THE PRESENCE OF CALCIUM IONS AND PHOSPHOLIPIDS.
CC -1- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and Villa.
CC -1- SUBUNIT: SYNTHESIZED AS A SINGLE CHAIN PRECURSOR, WHICH IS CLEAVED
CC INTO A LIGHT CHAIN AND A HEAVY CHAIN HELD TOGETHER BY A DISULFIDE
CC BOND. THE ENZYME IS THEN ACTIVATED BY THROMBIN, WHICH CLEAVES A
CC TETRADECAPEPTIDE FROM THE AMINO END OF THE HEAVY CHAIN; THIS
CC REACTION, WHICH OCCURS AT THE SURFACE OF ENDOTHELIAL CELLS, IS
CC STRONGLY PROMOTED BY THROMBOMODULIN.
CC -1- TISSUE SPECIFICITY: PLASMA; SYNTHESIZED IN THE LIVER.
CC -1- PTM: THE VITAMIN K-DEPENDENT, ENZYMATIC CARBOXYLATION OF SOME
CC GLU RESIDUES ALLOWS THE MODIFIED PROTEIN TO BIND CALCIUM.
CC -1- MISCELLANEOUS: CALCIUM ALSO BINDS, WITH STRONGER AFFINITY TO
CC ANOTHER SITE, BEYOND THE GLA DOMAIN. THIS GLA-INDEPENDENT BINDING
CC SITE IS NECESSARY FOR THE RECOGNITION OF THE
CC THROMBIN-THROMBOMODULIN COMPLEX.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: X64336; CAA45617.1; -
DR PIR: S18994; S18994.
DR PIR: S24312; S24312.
DR HSP: P04070; 1PCU.
DR MEROPS: S01.218; -
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR001314; Chymotrypsin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR002383; GLA_blood.
DR InterPro: IPR001254; Ser_protease_Try.
DR InterPro: IPR000294; VitK_dep_GLA.
DR Pfam: PF00008; EGF; 2.
DR Pfam: PF00089; trypsin; 1.
DR Pfam: PF00594; gla; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00001; GLABLOOD.
DR SMART: SM00179; EGF_CA; 1.
DR SMART: SM00001; EGF_Like; 1.
DR SMART: SM00069; GLA; 1.
DR SMART: SM00020; TRYPSIN; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 1.
DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Blood coagulation; Glycoprotein; Serine protease;
DR Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
DR EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
GN SIGNAL
FT 1 32 BY SIMILARITY.

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FT PROPEP 33 41 BY SIMILARITY.
FT CHAIN 42 196 PROTEIN C LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 199 461 PROTEIN C HEAVY CHAIN (BY SIMILARITY).
FT SITE 199 212 ACTIVATION PEPTIDE (BY SIMILARITY).
FT SITE 212 212 CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
FT DOMAIN 96 131 EGF-LIKE 1.
FT DOMAIN 135 175 EGF-LIKE 2.
FT DOMAIN 213 461 SERINE PROTEASE.
FT MOD_RES 47 47 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 48 48 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 55 55 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 57 57 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 61 61 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 66 66 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 67 67 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
FT MOD_RES 112 112 HYDROXYLATION (BY SIMILARITY).
FT ACT_SITE 254 254 CHARGE RELAY SYSTEM.
FT ACT_SITE 300 300 CHARGE RELAY SYSTEM.
FT ACT_SITE 402 402 CHARGE RELAY SYSTEM.
FT DISULFID 58 63 BY SIMILARITY.
FT DISULFID 91 110 BY SIMILARITY.
FT DISULFID 100 105 BY SIMILARITY.
FT DISULFID 104 119 BY SIMILARITY.
FT DISULFID 121 130 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT DISULFID 146 159 BY SIMILARITY.
FT DISULFID 161 174 BY SIMILARITY.
FT DISULFID 182 320 INTERCHAIN (BY SIMILARITY).
FT DISULFID 239 255 BY SIMILARITY.
FT DISULFID 373 387 BY SIMILARITY.
FT DISULFID 398 426 BY SIMILARITY.
FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 461 AA: 51912 MW: 8A4CF93664EDACD5 CRC64:

```

Alignment Scores:

Pred. No.:	Length:	Matches:
77.5	461	7
Score:	7.00	Conservative: 0
Percent Similarity:	100.00%	Mismatches: 0
Best Local Similarity:	100.00%	Indels: 0
Query Match:	2.86%	Gaps: 0

US-09-817-318-1 (1-780) x PRTC_RAT (1-461)

OY 454 TCCTGAAATCACCACAACTG 474

DB 455 SerLeuysSerProLysLeu 461

RESULT 40

FMNL_HUMAN

ID FMNL_HUMAN STANDARD: PRT: 463 AA.

AC 095466: 096H10:

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Formin-like protein (Protein C17orf1).

GN FMNL OR C17ORF1B OR C17ORF1.

OS Homo sapiens (Human).

OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominiidae: Homo.

```

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99013435; PubMed=9799091;
RA Aronsson F.C., Magnusson P., Andersson B., Karsten S.L., Shibasaki Y.,
RA London C.L., Goate A.M., Brookes A.J.;
RT "The NIX protein kinase and C17orf1 genes: chromosomal mapping, gene
RT structures and mutational screening in frontotemporal dementia and
RT parkinsonism linked to chromosome 17."
RL Hum. genet. 103:340-345(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph. and Placenta;
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -I- TISSUE SPECIFICITY: Expressed in heart, brain, placenta, lung,
CC liver, skeletal muscle, kidney, and pancreas.
CC -I- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 2 (FH2) DOMAIN.
CC -----
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CC -----
CC EMBL: AJ008112; CA007870.1; -
CC EMBL: BC001710; AAH01710.1; -
CC EMBL: BC009000; AAH09000.1; -
CC GeneW: HGNC:1212; FMNL.
CC MIM: 604656; -
CC InterPro: IPR003104; FH2.
CC Pfam: Pf02181; FH2; 1.
CC SMART: SM00498; FH2; 1.
FT DOMAIN 1 426 FH2.
FT CONFLICT 229 232 MKSP -> SPTS (IN REF. 2; AAH09000).
SQ SEQUENCE 463 AA: 52433 MW: 17E9CA5A28BEA33E CRC64:

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Alignment Scores:

Pred. No.:	Length:	Matches:
77.5	463	7
Score:	7.00	Conservative: 0
Percent Similarity:	100.00%	Mismatches: 0
Best Local Similarity:	100.00%	Indels: 0
Query Match:	2.92%	Gaps: 0

US-09-817-318-1 (1-780) x FMNL_HUMAN (1-463)

OY 628 GTACTTCTGATTTATCCCTG 608

DB 457 ValThrSerAspLeuSerLeu 463

RESULT 41

AP54_YEAST

ID AP54_YEAST STANDARD: PRT: 475 AA.

AC 000776:

DT 01-APR-1993 (Rel. 25, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Clathrin coat assembly protein AP54 (Clathrin coat associated protein

DE AP54) (Golgi adaptor Ap-1 54 kDa protein) (HA1 54 kDa subunit)

DE (Clathrin assembly protein complex 1 medium chain).

GN APM1 OR YAP54 OR YPL259C OR P0394.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes: Saccharomycetales: Saccharomycetaceae: Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92104180; PubMed=1761056;

RA Nakayama Y., Goebel M., O'Brien G.B., Lemmon S., Pingchang C.E.,

RA Kirchhausen T.;
 RT "The medium chains of the mammalian clathrin-associated proteins have
 a homolog in yeast."
 RL Eur. J. Biochem. 202:569-574(1991).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-S288c / AB972;
 RX MEDLINE=97313271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Anseorge W.,
 Araujo R., Aparicio A., Barrell B.G., Badcock K., Barnes V.,
 Botstein D., Bowman S., Bruchner M., Carpenter J., Cherry J.M.,
 Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
 Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,
 Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
 Hunkle-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
 Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
 Marathe R., Messenguy F., Mewes H.-W., Mitalpali S., Moestl D.,
 Mueller Auer S., Namach A., Neutwich U., Oefner P., Pearson D.,
 Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
 Scherens B., Schramm S., Schroeder M., Sidcu A.M., Tettelin H.,
 Ureterazulu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
 Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,
 Zhong W.W., Zollner A., Vo D.H., Hani J.,
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI."
 RL Nature 387:103-105(1997).
 CC -1- FUNCTION: COMPONENT OF THE ADAPTOR COMPLEXES WHICH LINK CLATHRIN
 TO RECEPTORS IN COATED VESICLES. CLATHRIN-ASSOCIATED PROTEIN
 COMPLEXES ARE BELIEVED TO INTERACT WITH THE CYTOPLASMIC TAILS OF
 MEMBRANE PROTEINS, LEADING TO THEIR SELECTION AND CONCENTRATION.
 CC AP57 IS PROBABLY A SUBUNIT OF THE GOLGI MEMBRANE ADAPTOR.
 CC -1- SUBUNIT: ASSEMBLY SUBUNIT OF THE GOLDI MEMBRANE ADAPTOR
 CC COMPOSED OF TWO LARGE CHAINS (GAMMA AND BETA'), A MEDIUM CHAIN
 CC (AP54) AND A SMALL CHAIN (AP19).
 CC -1- SUBCELLULAR LOCATION: COATED VESICLE.
 CC -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
 CC FAMILY.

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CC EMBL: X60288; CAA4282.1; -
 DR EMBL: 273615; CAA97989.1; -
 DR PIR: S17028; S17028.
 DR TRANSFAC: T03713; -
 DR SGD: S0006180; APM1.
 DR InterPro: IPR001392; Clathrn_med.
 DR Pfam: PF00928; Adap_comp_sub.1.
 DR PRINTS: PRO0314; CLATHRINADPT.
 DR PROSITE: PS00990; CLAT_ADAPTOR_M_1.1.
 DR PROSITE: PS00991; CLAT_ADAPTOR_M_2.1.
 KW Coated pits; Phosphorylation.
 CC FT CONFLICT 214 214 M -> I (IN REF. 1).
 CC FT CONFLICT 216 216 D -> H (IN REF. 1).
 CC FT CONFLICT 222 222 N -> K (IN REF. 1).
 CC FT CONFLICT 433 433 P -> R (IN REF. 1).
 CC FT CONFLICT 440 440 I -> M (IN REF. 1).
 CC FT CONFLICT 450 450 MISSING (IN REF. 1).
 CC FT CONFLICT 450 450 MISSING (IN REF. 1).
 SQ SEQUENCE 475 AA: 53873 MW: 6611153845921C CRC64;

Alignment Scores:

Pred. No.: 77.1 Length: 475
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x AP54_YEAST (1-475)
 Oy 283 TGTGATGTTAATGTTCAAGTC 263
 ||||||||||||||||
 Db 318 CysAspValAsnValGlnVal 324

RESULT 42

YDE5_SCHPO
 ID YDE5_SCHPO STANDARD: PRT: 486 AA.
 AC 010439;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable peptidase Cl2B10.05 (EC 3.4.-.-).
 GN SPAC12B10.05.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 OX [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor A., Cronin A., Davis P., Felwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald D., Odell C.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odel C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehnach E., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambut R., Purnelle B.,
 RA Goffeau A., Gadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Kochet M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Pausen P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24B.
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 CC or send an email to license@isb-sib.ch).

CC EMBL: Z70721; CAA4695.1; -
 DR HSSP: P15034; IAI6.
 DR MEROPS: M24_026; -
 DR InterPro: IPR000994; Peptidase_M24.
 DR InterPro: IPR001311; Xaa-Pro_Pepts.
 DR Pfam: PF00557; Peptidase_M24.1.
 DR PROSITE: PS00491; PROLINE_PEPTIDASE; 1.
 KW Hypothetical protein; Hydrolase.
 SQ SEQUENCE 486 AA: 55140 MW: 113B6FD4758D989B CRC64;

Alignment Scores:

Pred. No.: 76.8 Length: 486
 Score: 7.00 Matches: 7

Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 2.92%
 DB: 1
 Gaps: 0

US-09-817-318-1 (1-780) x YDE5_SCHPO (1-486)

OY 725 ATATTACACGAGCAATTA 705
 ||||||||||||||||
 Db 52 ILEuclnProGlyGluLeu 58

RESULT 43

VGA_BPPHX STANDARD; PRT; 513 AA.
 AC P03631:
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE A and A* proteins (GPA).
 GN A.
 OS Bacteriophage phi-X174.
 OC Viruses; ssDNA viruses; Microviridae; Microvirus.
 OX NCBI_TaxID=10847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=77171175; PubMed=870828;
 RA Sanger F., Air G.M., Barrell B.G., Brown N.L., Coulson A.R.,
 RA Fiddes J.C., Hutchison C.A. III, Slocombe P.M., Smith M.;
 RT "Nucleotide sequence of bacteriophage phi X174 DNA";
 RL Nature 265:687-695(1977).
 RN [2]
 RP REVISIONS.
 RX MEDLINE=79091165; PubMed=731693;
 RA Sanger F., Coulson A.R., Friedmann T., Air G.M., Barrell B.G.,
 RA Brown N.L., Fiddes J.C., Hutchison C.A. III, Slocombe P.M., Smith M.;
 RT "The nucleotide sequence of bacteriophage phiX174";
 RL J. Mol. Biol. 125:225-246(1978).
 RN [3]
 RP FUNCTION OF A AND A*
 RX MEDLINE=80027245; PubMed=158588;
 RA Ikeda J., Ydelevich A., Shimamoto N., Hurwitz J.;
 RT "Role of polymeric forms of the bacteriophage phi X174 coded gene A
 protein in phi XRFI DNA cleavage";
 RL J. Biol. Chem. 254:9416-9428(1979).
 RN [4]
 RP ACTIVE SITE TYROSINE.
 RX MEDLINE=86232554; PubMed=2940511;
 RA van Mansfield A.D.M., van Teeffelen H.A.A.M., Baas P.D., Jansz H.S.;
 RT "Two juxtaposed tyrosyl-OH groups participate in phi X174 gene A
 protein catalysed cleavage and ligation of DNA";
 RL Nucleic Acids Res. 14:4229-4238(1986).
 CC -1- FUNCTION: THE A PROTEIN IS A SPECIFIC ENDONUCLEASE THAT CLEAVES
 THE VIRAL STRAND OF SUPERSTWISTED, CLOSED CIRCULAR DNA AT A UNIQUE
 SITE IN THE A GENE. THE A PROTEIN ALSO CAUSES RELAXATION OF
 CC SUPERSTWISTED DNA AND FORMS A COMPLEX WITH VIRAL DNA THAT HAS A
 CC DISCONTINUITY IN GENE A OF THE VIRAL STRAND.
 CC -1- FUNCTION: GENE A* PROTEIN IS FORMED FROM A NATURAL INITIATION SITE
 WITHIN THE A GENE. IT BINDS TO DOUBLE-STRANDED DNA AND PREVENTS
 CC THEIR HYDROLYSIS BY NUCLEASES.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (PROBABLY).
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 CC or send an email to license@isb-sib.ch).

DR EMBL: V01128; CAA24351.1; -;
 DR EMBL: J02482; AAA32570.1; -;
 DR EMBL: J02482; AAA32571.1; ALT_INIT.
 DR PIR: A04239; ZABPF4.
 KM Hydrolase; Nuclease; Endonuclease; DNA-binding; Zinc-finger.

FT CHAIN 1 513 PROTEIN A (BY SIMILARITY WITH G4).
 FT CHAIN 173 513 PROTEIN A* (BY SIMILARITY WITH G4).
 FT ZN-FING 246 268 POTENTIAL.
 FT BINDING 347 347 TO DNA (WHEN NICKING OCCURS).
 SO SEQUENCE 513 AA; 58718 MW; EF2D4DC93BC8072 CRC64;

Alignment Scores:

Pred. No.: 76 Length: 513
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.92% Indels: 0
 DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x VGA_BPPHX (1-513)

OY 234 GTCACACATTTTGTAGAAA 214
 ||||||||||||||||
 Db 132 ValThrGlnPheCysArgLys 138

RESULT 44

SC59_YEAST STANDARD; PRT; 519 AA.
 AC P20048:
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dolichol kinase (EC 2.7.1.108).
 GN SEC59 OR YMR013C OR YMR270.17C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89261723; PubMed=2657387;
 RA Bernstein M., Kepes F., Schekman R.;
 RT "Sec59 encodes a membrane protein required for core glycosylation in
 RT Saccharomyces cerevisiae";
 RL Mol. Cell. Biol. 9:1191-1199(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=S288C / AB972;
 RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP CHARACTERIZATION.
 RX STRAIN=S288C;
 RC MEDLINE=92357761; PubMed=1323123;
 RA Heller L., Orlean P., Adair W.L. Jr.;
 RT "Saccharomyces cerevisiae sec59 cells are deficient in dolichol
 RT kinase activity";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:7013-7016(1992).
 CC -1- FUNCTION: INVOLVED IN THE SYNTHESIS OF N-LINKED AND O-LINKED
 WHICH IS REQUIRED AND FOR THAT OF GPI ANCHORS. IT IS REQUIRED FOR
 CC OLIGOSACCHARIDES AND FOR AN ESSENTIAL ROLE IN CELLULAR METABOLISM.
 CC SPORE GERMINATION. HAS AN ESSENTIAL ROLE IN CELLULAR METABOLISM.
 CC -1- CATALYTIC ACTIVITY: cnp + dolichol = CDP + dolichyl phosphate.
 CC -1- PATHWAY: Glycosylation.
 CC -1- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM MEMBRANE (PROBABLY).
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DR EMBL: M25779; AAA35033.1; -;
 DR EMBL: 248613; CAA88530.1; -;
 DR PIR: J00124; J00124.
 SGD: S0004615; SEC59.

DR InterPro: IPR002741; DUF56.
DR Pfam: PF01879; DUF56; 1.
KW Endoplasmic reticulum; Membrane; Transferase; Kinase.
FT CARBOHYD 326 326 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 519 AA; 58906 MW; 2C75B6F175B8FF06 CRC64;

Alignment Scores:
Pred. No.: 75.8 Length: 519
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x SC59_YEAST (1-519)

OY 667 GTGTAATTCATTACTGAGC 687
Db 185 ValtHeasnerLeuSer 191
|||||

RESULT 45
VGA_BPS13
ID VGA_BPS13 STANDARD; PRT; 522 AA.
AC P07928;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE A', A and A* proteins (GPA).
GN A.
OS Bacteriophage S13.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10844;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86165869; PubMed=3007293;
RA Lau P.C.K., Spencer J.H.;
RT "Nucleotide sequence and genome organization of bacteriophage S13
DNA";
RL Gene 40:273-284(1985).
RN [2]
RP SEQUENCE OF 269-333 FROM N.A.
RX MEDLINE=78011668; PubMed=909772;
RA Grosveld F.G., Spencer J.H.;
RT "The nucleotide sequence of two restriction fragments located in the
gene AB region of bacteriophage S13";
RL Nucleic Acids Res. 4:2235-2252(1977).
CC -!- FUNCTION: THE A PROTEIN IS A SPECIFIC ENDONUCLEASE THAT CLEAVES
THE VIRAL STRAND OF SUPERTWISTED, CLOSED CIRCULAR DNA AT A UNIQUE
SITE IN THE A GENE. THE A PROTEIN ALSO CAUSES RELAXATION OF
SUPERTWISTED DNA AND FORMS A COMPLEX WITH VIRAL DNA THAT HAS A
DISCONTINUITY IN GENE A OF THE VIRAL STRAND.
CC -!- FUNCTION: GENE A* PROTEIN IS FORMED FROM A NATURAL INITIATION SITE
WITHIN THE A GENE. IT BINDS TO DOUBLE-STRANDED DNA AND PREVENTS
THEIR HYDROLYSIS BY NUCLEASES.

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CC -----

DR EMBL: M14428; AAA32581.1; -;
DR EMBL: M14428; AAA32582.1; -;
DR EMBL: M14428; AAA32583.1; -;
DR PIR: J50450; J50450.
KW Hydrolyase; Nuclease;
FT CHAIN 1 522 PROTEIN A'.
FT CHAIN 10 522 PROTEIN A.
FT CHAIN 182 522 PROTEIN A*.
FT ZN_FING 255 277 POTENTIAL.

FT BINDING 356 356 TO DNA (WHEN NICKING OCCURS)
FT
SQ SEQUENCE 522 AA; 59882 MW; CE9DE9AC679403A2 CRC64;
(BY SIMILARITY).

Alignment Scores:
Pred. No.: 75.8 Length: 522
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x VGA_BPS13 (1-522)

OY 234 GTCACACAAATTTGTAGAAA 214
Db 141 ValtHrcInphecysArglys 147
|||||

Search completed: February 4, 2003, 07:18:19
Job time : 26.5 secs

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 4, 2003, 07:17:33 ; Search time 43 Seconds
(without alignments)
3487.667 Million cell updates/sec

```
Title: US-09-817-318-1
Perfect score: 245
Sequence: 1 aatcactgtctctctaag.....taagcagaaaaaaaaa 780
```

Scoring table:	
OLIGO	
Xgapop 60.0 ,	Xgapext 60.0
Ygapop 60.0 ,	Ygapext 60.0
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 283224 seqs, 96134422 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565536

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 45 summaries

Command line parameters:

```
MODEL=lrtime+np,model=05917318/runat,04022003,071723.6638/app.query,fasta_1.965
-O=cn2,1/USPO.spool/US0917318
-DB=PIR.73 -QEXT=fasta -SUFFIX=grp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=0101 -TRANS=ham40,0,cd1 -LIST=45
-DUALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFWT=Pto
-NOR-ext -HEAPSIZE=500 -MILEN=0 -MAXLEN=2000000000
-USER=050917318 GCN=1,1,48 -runat,04022003,071723.6638 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAB -TARGETQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THEADS=1 -XCAPD=60 -FGAPEXT=60 -FGAPD=6 -FGAPEXT=7
-YGAPD=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
```

Database :

```
PIR_73: *
1:  pir1: *
2:  pir2: *
3:  pir3: *
4:  pir4: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	DB	ID	Description
C 1	2	8	3.3	145	2	G81263	probable periplasm
C 2	8	8	3.3	225	2	T04451	hypothetical prote
C 3	8	8	3.3	266	2	C75613	probable molybden
C 4	8	8	3.3	341	2	T46153	hypothetical prote
C 5	8	8	3.3	454	2	T01400	translation elonga
C 6	8	8	3.3	528	2	S67624	ASMA protein
C 7	8	8	3.3	607	2	C64220	oligoendopeptidase
C 8	8	8	3.3	866	2	C97662	hypothetical prote
C 9	8	8	3.3	866	2	AF2886	conserved hypot
C 10	8	8	3.3	963	2	H85015	hypothetical prote
C 11	8	8	3.3	1613	2	H82193	conserved hypot
C 12	7	7	2.9	20	2	A60897	class I histocompa
C 13	7	7	2.9	31	2	S58771	NADH2 dehydrogena
C 14	7	7	2.9	76	2	E64453	hypothetical prote

C	15	7	2.9	91	2	T42310	hypothetical prote
C	16	7	2.9	102	2	A02196	MHC class I histoc
C	17	7	2.9	105	1	A46264	thioredoxin 1 - SL
C	18	7	2.9	111	2	A02197	MHC class I histoc
C	19	7	2.9	134	2	I48639	neurotoxin homolog
C	20	7	2.9	146	2	T13311	hypothetical prote
C	21	7	2.9	147	2	T18586	hypothetical prote
C	22	7	2.9	153	2	G87632	hypothetical prote
C	23	7	2.9	154	2	I58201	MHC class I antige
C	24	7	2.9	158	2	D90066	hypothetical prote
C	25	7	2.9	172	2	A35145	transcripton repr
C	26	7	2.9	173	1	JT0302	DNA-directed RNA p
C	27	7	2.9	173	2	A39022	acetylcholinestera
C	28	7	2.9	174	2	S45548	hypothetical prote
C	29	7	2.9	175	2	D75514	hypothetical prote
C	30	7	2.9	199	2	S14981	extensin class I (
C	31	7	2.9	206	2	T31585	hypothetical prote
C	32	7	2.9	211	2	T17228	hypothetical prote
C	33	7	2.9	219	2	T45597	hypothetical prote
C	34	7	2.9	219	2	S59134	probable zinc fing
C	35	7	2.9	220	2	S40931	hypothetical prote
C	36	7	2.9	222	2	A10781	GTP cyclohydrolase
C	37	7	2.9	224	2	D89836	hypothetical prote
C	38	7	2.9	231	2	G70000	two-component resp
C	39	7	2.9	231	2	G84138	two-component resp
C	40	7	2.9	235	2	S43513	hemoglobin linker
C	41	7	2.9	237	2	D70032	two-component resp
C	42	7	2.9	238	2	A81422	probable RNA polym
C	43	7	2.9	245	1	A38379	phosducin, retinal
C	44	7	2.9	245	2	G81297	hypothetical prote
C	45	7	2.9	251	2	T17397	vrio protein - Dic

ALIGNMENTS

RESULT 1
G81263
Probable periplasmic protein Cj1666c [imported] - Campylobacter jejuni (strain NCTC 11697)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence-revision 31-Mar-2000 #text-change 03-Jun-2002
C:Accession: G81263
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chittenden, R.; Coulthurst, S.; Davies, A.P.; De Jong, P.; Fiegler, H.; Fraser, A.R.; Harris, D.S.; Holt, K.E.; Jones, A.P.; Kearse, M.; McQuinn, K.; Miller, J.; Park, J.; Paulsen, O.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Van Vlier, A.; Whitehead, S.; Barrell, A.N.G.
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A:Reference number: AB1250; PMID:20150912; PMID:10688204
A:Accession: G81263
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <PAR>
A:Cross-references: GB:AL139079; GB:AL111168; NID:66968971; PIDN:CAW73653.1; PID:969f
A:Experimental source: serotype O2, strain NCTC 11697
C:Genetics:
A:Gene: Cj1666c
Superfamily: Campylobacter jejuni probable periplasmic protein Cj1666c

Alignment Scores:

Pred. No.:	13.5	length:	145
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	3.27%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x G81263 (1-145)

QY 651 TATGGTATTATAGGTGATAA 674

Db 136 TYRGLTYRPHETGLYASPLYS 143

RESULT 2
T04451
hypothetical protein F4D1.60 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 26-Aug-1999
C:Accession: T04451
R:Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansgorge, W.; Hohnel, J.; Mewes, H.W.
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15360
A:Accession: T04451
A:Molecule type: DNA
A:Residues: 1-235 <BEV>
A:Cross-references: EMBL:AL022537
A:Experimental source: cultivar Columbia; BAC clone F4D11
C:Genetics:
A:Map position: 4
A:Insertions: 66/2; 104/3; 196/3
A:Note: F4D11.60
C:Superfamily: Arabidopsis hypothetical protein F4D11.60

Alignment Scores:
Pred. No.: 12.9 Length: 235
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T04451 (1-235)

QY 482 CATAAATCAGTTGGCTGATTTC 459
|||||
Db 21 HistylleSerleuGlyAspHe 28

RESULT 3
C75613
probable molybdenum ABC transporter, permease protein - Deinococcus radiodurans (strain
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: C75613
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75613
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <WHI>
A:Cross-references: GB:AE001862; GB:AE001825; NID:g6460468; PIDN:AAF12201.1; PID:g6460468
A:Experimental source: strain R1
C:Genetics:
A:Gene: DRA0168
A:Map position: 2
C:Superfamily: maltose transport protein malG

Alignment Scores:
Pred. No.: 12.7 Length: 266
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x C75613 (1-266)

QY 646 ATACTTGTATTGACAGTAAC 623
|||||
Db 61 IlleThleuLeuThrValTrn 68

RESULT 4
T46153
hypothetical protein T3A5.140 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 18-Feb-2000

C:Accession: T46153; T08397
R:Boecker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, F.; S
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z23024
A:Accession: T46153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-341 <BL0>
A:Cross-references: EMBL:AL132979
A:Experimental source: cultivar Columbia; BAC clone T3A5
R:Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16409
A:Accession: T08397
A:Molecule type: DNA
A:Residues: 1-341 <QUE>
A:Cross-references: EMBL:AL049862; GSPDB:GN00061; ATSP:FL18B3.40
A:Experimental source: cultivar Columbia; BAC clone FL18B3
C:Genetics:
A:Gene: ATSP:FL18B3.40
A:Map position: 3
A:Note: T3A5.140

Alignment Scores:
Pred. No.: 12.4 Length: 341
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.27% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T46153 (1-341)

QY 98 AGTAACTTTATTTATTTATCC 121
|||||
Db 3 SerlySPhelleuTrleuSer 10

RESULT 5
T01400
translation elongation factor EF-Tu precursor, mitochondrial - Arabidopsis thaliana
N:Alternate names: protein T419.19
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001
C:Accession: T01400; S62701
R:Parnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.; Schutz, K.;
submitted to the EMBL data library, May 1998
A:Description: Genomic sequence of BAC T419 from Arabidopsis thaliana, chromosome IV,
A:Reference number: Z14314
A:Accession: T01400
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-454 <PAR>
A:Cross-references: EMBL:AF069442; NID:g3242970; PIDN:MAC79113.1; PID:g3924612
A:Experimental source: cultivar Columbia
R:Kuhlman, P.; Palmer, J.D.
Plant Mol. Biol. 29, 1057-1070, 1995
A:Title: Isolation, expression, and evolution of the gene encoding mitochondrial elon
A:Reference number: S62701; MUID:96145515; PMID:8555448
A:Accession: S62701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'MEEPVREDIDLRVSSDTIGW', 8, 'EFAAA', 11-309, 'CST', 313-454 <RUH>
A:Cross-references: EMBL:X89227; NID:g1149570; PIDN:CAA61511.1; PID:g1149571
C:Genetics:
A:Gene: tu1m
A:Map position: 4
A:Genome: nuclear
A:Insertions: 64/2; 89/3; 120/3; 145/3; 180/3; 211/1; 279/3; 307/3; 330/3; 351/3; 432/1
A:Note: T419.19
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu hom
C:Keywords: GTP binding; mitochondrion; nucleotide binding; P-loop; protein biosynthe
F1-55/Domain: transit peptide (mitochondrion) #status predicted <TRN>
F1-56-454/Product: translation elongation factor EF-Tu #status predicted <MAT>

F:68-194/Domain: translation elongation factor Tu homology <ETU>
F:74-81/Region: nucleotide-binding motif A (P-loop)
F:191-194/Region: GTP-binding NKXD motif
F:229-231/Region: GTP-binding SAK/L motif
F:80,81,117,191,192,194,229/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #st

Alignment Scores:

Pred. No.:	12.1	Length:	454
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.27%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x T01400 (1-454)

OY 587 AAAACATATTAGTAAATGGCAG 610

Db 323 LysLysIleLeuAspAsnGlyGln 330

RESULT 6

S67624

ASM4 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D2420; protein YDL088c

C:Species: Saccharomyces cerevisiae

C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 29-Oct-1999

C:Accession: S67624; S67630; S51486; S67429

R:Wambutt, R.; Wedler, H.; Wedler, E.; Scharfe, M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67608

A:Accession: S67624

A:Molecule type: DNA

A:Residues: 1-528 <WAM>

A:Cross-references: EMBL:Z74136; NID:g1431115; PIDN:CAA98654.1; PID:e253023; PID:g143111

A:Experimental source: strain S288C

R:Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bc

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67629

A:Accession: S67630

A:Molecule type: DNA

A:Residues: 1-528 <BAL>

A:Cross-references: EMBL:Z74136; NID:g1431115; PIDN:CAA98654.1; PID:e253023; PID:g143111

A:Experimental source: strain S288C

R:Giot, L.; Simon, M.; Dubois, C.; Faye, G.

Mol. Gen. Genet. 246, 212-222, 1995

A:Title: Suppressors of thermosensitive mutations in the DNA polymerase delta gene of Sa

A:Reference number: S51486; MOID:95166178; PMID:7862092

A:Accession: S51486

A:Molecule type: DNA

A:Residues: 1-113, 'L', 115-445, 'LPVMLVIOIFQVQ' <GIO>

A:Cross-references: EMBL:X76709; NID:g732940; PIDN:CAA54130.1; PID:g732941

R:Poskovic, J.; Salic, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine

submitted to the EMBL Data Library, February 1996

A:Reference number: S67429

A:Accession: S67429

A:Molecule type: DNA

A:Residues: 1-528 <ROS>

A:Cross-references: EMBL:X95644; NID:g1199535; PIDN:CAA64923.1; PID:e223198; PID:g119955

C:Genetics:

A:Gene: SGD:ASM4

A:Cross-references: SGD:S0002246; MIPS:YDL088c

A:Map position: 4L

Alignment Scores:

Pred. No.:	11.9	Length:	528
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.27%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x S67624 (1-528)

OY 670 ATAAATTCATTACTGACCAATTC 693
|||||
Db 170 IleaSerLeuSerAsnSnp 177

RESULT 7

C64220

oligodeopeptidase F homolog - Mycoplasma genitalium

C:Species: Mycoplasma genitalium

C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 07-Dec-1999

C:Accession: C64220

R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.

M.; Fuhrmann, J.; Nguyen, D.; Ullrich, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick,

C.A.; Venter, J.C.

Science 270, 397-403, 1995

A:Title: The minimal gene complement of Mycoplasma genitalium.

A:Reference number: A64200; MOID:96026346; PMID:7569993

A:Accession: C64220

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-607 <TIGR>

A:Cross-references: GB:U39695; GB:L43967; NID:g1045833; PID:g1045867; TIGR:MG183

A:Experimental source: strain G-37

C:Genetics:

C:Superfamily: oligodeopeptidase F

Alignment Scores:

Pred. No.:	11.7	Length:	607
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.33%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x C64220 (1-607)

OY 150 TTGCTATTATGCTATTATGACTA 127

Db 419 LeuLeuLeuCysTyrTyrGluLeu 426

RESULT 8

C97662

hypothetical protein AGR_C_4580 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens

C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002

C:Accession: C97662

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouzollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappae, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: C97662

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-866 <KUR>

A:Cross-references: GB:AE007869; PIDN:AK88252.1; PID:g15157710; GSPDB:GN00169

C:Genetics:

A:Gene: AGR_C_4580

A:Map position: circular chromosome

Alignment Scores:

Pred. No.:	11.3	Length:	866
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.27%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x C97662 (1-866)

OY 428 GTTCCTTGGCTATTAATGAACA 451

Db 376 ValProLeuProIleIleGlnAla 383

RESULT 9

AF2886

conserved hypothetical protein Atu2521 [imported] - *Agrobacterium tumefaciens* (strain C5C:Species: *Agrobacterium tumefaciens*

C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002

C:Accession: AF2886

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L

erage, G.; Gilet, M.; Grant, C.; Genthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: AF2886

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-866 <KUR>

A:Cross-References: GB:AE008688; PIDN:AAL43508.1; PID:g17741016; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Map position: circular chromosome

Alignment Scores:

Pred. No.: 11.3

Score: 8.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.27%

DB: 2

US-09-817-318-1 (1-780) x AF2886 (1-866)

QY 428 GTTCCTTGGCTATTAATGAGCA 451

|||||

Db 376 ValProLeuProIleIleGluAla 383

RESULT 10

H85015

hypothetical protein AT4G01210 [imported] - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001

C:Accession: H85015

R:anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.

A:Reference number: AB5001; MUID:20083488; PMID:10617198

A:Accession: H85015

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-963 <STO>

A:Cross-References: GB:NC_001268; NTD:g7267618; PIDN:CA80930.1; GSPDB:GN00140

A:Gene: AT4G01210

A:Map position: 4

C:Superfamily: *Arabidopsis thaliana* hypothetical protein A_IG002N01.24

Alignment Scores:

Pred. No.: 11.2

Score: 8.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.33%

DB: 2

US-09-817-318-1 (1-780) x H85015 (1-963)

QY 348 AGAAGAGCTCACTGCAAAATT 325

|||||

Db 730 ArgLysGluSerLeuSerIle 737

RESULT 11

E82193

conserved hypothetical protein VC1492 [imported] - *Vibrio cholerae* (strain N16961 serC:Species: *Vibrio cholerae*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: E82193

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.

Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: AB2035; MUID:20406833; PMID:10952301

A:Accession: E82193

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1613 <HEI>

A:Cross-References: GB:AE004352; GB:AE003852; NTD:g9655990; PIDN:AAF94647.1; GSPDB:GN

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1492

A:Map position: 1

Alignment Scores:

Pred. No.: 10.7

Score: 8.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 3.33%

DB: 2

US-09-817-318-1 (1-780) x E82193 (1-1613)

QY 254 AGAGTAAAGCTGTAAGCTGCA 231

|||||

Db 264 ArgValArgSerValLysLeuSer 271

RESULT 12

A60897

class I histocompatibility antigen H-2K(d) alpha chain, alternate splice form - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 07-May-1999

C:Accession: A60897

R:Abu-Hadid, M.M.; Fujii, H.; Sood, A.K.

Mol. Immunol. 25, 739-749, 1988

A:Title: Identification of an alternatively spliced K(d) and the Qa-6(d) mRNAs by us1

A:Reference number: A60897; MUID:89039921; PMID:3141798

A:Accession: A60897

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-20 <ABU>

Alignment Scores:

Pred. No.: 192

Score: 7.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 2.92%

DB: 2

US-09-817-318-1 (1-780) x A60897 (1-20)

QY 625 ACTCTGATTATCCCTGCC 605

|||||

Db 3 ThrSerAspLeuSerLeuPro 9

RESULT 13

S58771

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - *Pythium oligandrum* mitochondC:Species: *Pythium oligandrum*

C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 03-Jun-2002

C:Accession: S58771

R:Martin, F.N.

Curr. Genet. 28, 225-234, 1995

A:Title: Linear mitochondrial genome organization in vivo in the genus *Pythium*.
A:Reference number: S58771; MUID:96071191; PMID:8529268
A:Accession: S58771
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <MAR>
A:Cross-references: EMBL:U28355
C:Genetics:
A:Gene: nad4L
A:Genome: mitochondrion
A:Superfamily: NADH dehydrogenase (ubiquinone) chain 4L
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Alignment Scores:
Pred. No.: 184 Length: 31
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x S58771 (1-31)

OY 114 TATAAATAAAGTACTCTCA 94
|||||
DB 24 TyrlsTlleAsnLeuLeuSer 30

RESULT 14
E64453
hypothetical protein MJ1230 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: E64453
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: E64453
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-76 <BUL>
A:Cross-references: GB:U67563; GB:U77117; NID:g2826379; PIDN:AAB99236.1; PID:g1591861; T
C:Genetics:
A:Map position: REV1173464-1173234
A:Start codon: TTG

Alignment Scores:
Pred. No.: 168 Length: 76
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x E64453 (1-76)

OY 267 AAGTCATTGTGACAGATTAAG 247
|||||
DB 58 LysSerIleValLysSerLys 64

RESULT 15
T42310
hypothetical protein - phage SPPI
C:Species: phage SPPI
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C:Accession: T42310
R:Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A:Title: The complete nucleotide sequence and functional organization of *Bacillus subtilis*
A:Reference number: 222137; MUID:98094274; PMID:9434185

A:Accession: T42310
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-91 <ALO>
A:Cross-references: EMBL:X97918; PIDN:CAA6517.1

Alignment Scores:
Pred. No.: 165 Length: 91
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x T42310 (1-91)

OY 342 GAGTCACGTGCAAAATTCAT 322
|||||
DB 41 GluSerLeuSerLysIleHis 47

RESULT 16
A02196
MHC class I histocompatibility antigen alpha chain (version 2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 23-Jul-1999
C:Accession: A02196
R:Kress, M.; Giaros, D.; Khoury, G.; Jay, G.
Nature 306, 602-604, 1983
A:Title: Alternative RNA splicing in expression of the H-2K gene.
A:Reference number: A02196; MUID:84068207; PMID:6689056
A:Accession: A02196
A:Molecule type: mRNA
A:Residues: 1-102 <KR>
A:Cross-references: GB:K01762; NID:g199548; PIDN:AAA39655.1; PID:g387470
A:Experimental source: strain SWR, clone pH13
A:Note: this carboxyl-terminal fragment was translated from clone pH13, one of two R.
C:Genetics:
A:Insertions: 102/L
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: glycoprotein; heterodimer; transmembrane protein
F:78-102/Domain: Intracellular <INT>

Alignment Scores:
Pred. No.: 163 Length: 102
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x A02196 (1-102)

OY 625 ACTTCTGATTATGCCGCGCC 605
|||||
DB 92 ThrSerAspLeuSerLeuPro 98

RESULT 17
A46264
thioredoxin 1 - slime mold (*Dictyostelium discoideum*)
C:Species: *Dictyostelium discoideum*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A46264
R:Wetterauer, B.; Jacquot, J.P.; Veron, M.
J. Biol. Chem. 267, 9895-9904, 1992
A:Title: Thioredoxins from *Dictyostelium discoideum* are a developmentally regulated,
A:Reference number: A46264; MUID:92250653; PMID:1577820
A:Accession: A46264
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-105 <WET>
A:Cross-references: GB:M91384; NID:g167928; PIDN:AAA33258.1; PID:g167929
C:Superfamily: thioredoxin; thioredoxin homology
C:Keywords: redox-active disulfide

F;9-92/Domain: thioredoxin homology <THR>
F;32-35/Disulfide bonds: redox-active #status predicted

Alignment Scores:

Pred. No.: 163 Length: 105
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 1 Gaps: 0

US-09-817-318-1 (1-780) x A46264 (1-105)

OY 686 CTCAGTATGATTTATCACC 666

Db 45 LeuserAsngluPheIleThr 51

RESULT 18

A02197

MHC class I histocompatibility antigen alpha chain (version 1) - mouse (fragment)
C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 23-Jul-1999

C:Accession: A02197

R:Kress, M.; Glaros, D.; Khoury, G.; Jay, G.

Nature 306, 602-604, 1983

A:Title: Alternative RNA splicing in expression of the H-2K gene.

A:Reference number: A02196; PMID:84068207; PMID:6689056

A:Accession: A02197

A:Molecule type: mRNA

A:Residues: 1111 <KRE>

A:Cross-references: GB:K01445; NID:951328; PIDN:CAA24997.1; PID:951329

A:Experimental source: strain SMR, clone p88

A:Note: the authors translated the codon CCG for residue 107 as Ser

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein

F;78-111/Domain: Intracellular <INT>

Alignment Scores:

Pred. No.: 162 Length: 111
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x A02197 (1-111)

OY 625 ACTTCGATTTATCCCGCC 605

Db 92 ThrSerAspLeuSerLeuPro 98

RESULT 19

I48639

neurotoxin homolog - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999

C:Accession: I48639

R:Fleming, T.J.; O'Nuigin, C.; Malek, T.R.

J. Immunol. 150, 5379-5390, 1993

A:Title: Characterization of two novel Ly-6 genes. Protein sequence and potential structure

A:Reference number: I48639; PMID:93294293; PMID:8515066

A:Accession: I48639

A:Molecule type: DNA

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-134 <RES>

A:Cross-references: EMBL:X70922; NID:9394727; PIDN:CAA50270.1; PID:9817978

A:Gene: Ly-6F.1

A:Introns: 24/1; 63/1

C:Superfamily: Ly-6 antigen; Ly-6 homology

Alignment Scores:

Pred. No.: 159 Length: 134
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x I48639 (1-134)

OY 701 GTTTAATTCCTCGTTGTA 721

Db 11 ValLeuIleLeuValVal 17

RESULT 20

T13311

hypothetical protein 22 - Streptococcus phage phi-O1205

C:Species: Streptococcus phage phi-O1205

C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 18-Aug-2000

C:Accession: T13311

R:Stanley, E.; Fitzgerald, G.F.; Le Marrec, C.; Fayard, B.; van Sinderen, D.

Microbiology 143, 3417-3429, 1997

A:Title: Sequence analysis and characterization of phi O1205, a temperate bacteriophage

A:Reference number: Z17654; PMID:98048466; PMID:9387220

A:Accession: T13311

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-146 <STAS>

A:Cross-references: EMBL:U08974; NID:92444080; PID:92444102; PIDN:AACT9538.1

A:Experimental source: host Streptococcus thermophilus strain CNR21205

C:Superfamily: Streptococcus phage phi-O1205 hypothetical protein 22

Alignment Scores:

Pred. No.: 158 Length: 146
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T13311 (1-146)

OY 295 GTTACAAAGATAGTCAG 315

Db 34 ValTyrIlySarGlyLeuValys 40

RESULT 21

T18586

hypothetical protein 6R55.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T18586

R:Wallis, J.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z18992

A:Accession: T18586

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-147 <WIL>

A:Cross-references: EMBL:AL031222; PIDN:CAA20210.1; GSPDB:GN00028; CESP:6R55.2

A:Experimental source: clone 6R55

C:Genetics:

A:Gene: CESP:6R55.2

A:Map position: X

A:Introns: 50/2; 119/1

C:Superfamily: Caenorhabditis elegans hypothetical protein 6R55.2

Alignment Scores:

Pred. No.: 157 Length: 147
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T18586 (1-147)

OY 415 TTTTCTCTGAGTTACCTTT 435

Db 114 PheserServalSerSerphe 120

RESULT 22

G87632 hypothetical protein CC3097 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: G87632

R:Neuman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

n. J.; Ermlaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: AB7249; MUID:21173698; PMID:11259647

A:Accession: G87632

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1153 <STO>

A:Cross-references: GB:AE005673; NID:g13424753; PIDN:AAK25059.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC3097

Alignment Scores:

Pred. No.: 157 Length: 153

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.86% Indels: 0

DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x G87632 (1-153)

OY 227 TGTGTGACAGCTTACAGACC 247

Db 144 CysValThrAlaLeuGlnThr 150

RESULT 23

158201 MHC class I antigen - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000

C:Accession: 158201

R:Jalanne, J.

Nucleic Acids Res. 10, 1039-1049, 1982

A:Title: Comparison of nucleotide sequences of mRNAs belonging to the mouse h-2 multigen

A:Reference number: 158201; MUID:82150234; PMID:6278432

A:Accession: 158201

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-164 <RES>

A:Cross-references: GB:J00395; NID:g199338; PIDN:AAA39579.1; PID:g387446

C:Superfamily: class I histocompatibility antigen; immunoglobulin homology

F:13-78/Domain: immunoglobulin homology <IMM>

Alignment Scores:

Pred. No.: 156 Length: 164

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.92% Indels: 0

DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x 158201 (1-164)

OY 625 ACTTGTGATTTATCCCTGCC 605

Db 145 ThrSerAspSerLeuPro 151

RESULT 24

D90066

hypothetical protein truncated-SA [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: D90066

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, I

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: AB9758; MUID:21311952; PMID:11418146

A:Accession: D90066

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-168 <KUR>

A:Cross-references: GB:BA000018; PID:g13702553; PIDN:BA943694.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: truncated-SA

Alignment Scores:

Pred. No.: 155 Length: 168

Score: 7.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.86% Indels: 0

DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x D90066 (1-168)

OY 704 TTAATTCCTCGTTGTAATA 724

Db 10 LeuIleuLeuValIle 16

RESULT 25

A35145

transcription repressor of sporulation, septation and degradation paia - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 20-Jun-2000

C:Accession: A35145; E69671

R:Honjo, M.; Nakayama, A.; Fukazawa, K.; Kawamura, K.; Ando, K.; Horii, M.; Furutani, J.

Bacteriol. 172, 1783-1790, 1990

A:Title: A novel Bacillus subtilis gene involved in negative control of sporulation

A:Reference number: A35145; MUID:90202692; PMID:2108124

A:Accession: A35145

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-172 <HON>

A:Cross-references: GB:M36471; NID:g143283; PIDN:AAA22638.1; PID:g143284

A:Experimental source: strain M168

R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Be

C.; Bron, S.; Brouillet, S.; Buschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Ga

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hult, I

Koehler, P.; Koningsstein, G.; Krogh, S.; Kuno, M.; Kurita, K.; Lapidus, A.; Lardinc

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portier

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scani

A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sc

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Toiron, A.; Tosato, V.; Uchiya

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: E69671

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-26, 'T', '28-172 <KUN>

A:Cross-references: GB:299120; GB:AL009126; NID:g2635613; PIDN:CAB15205.1; PID:g26357

A:Experimental source: strain 168

C:Genetics:
A:Gene: pailA
C:Superfamily: Bacillus subtilis transcription regulator
C:Keywords: DNA binding; transcription regulation

Alignment Scores:

Pred. No.:	155	Length:	172
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.92%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x A35145 (1-172)

OY 504 TCTTCCAAAGCATGGCTT 484

Db 101 SerpneGlnYshSgLYleu 107

RESULT 26

JT0302 DNA-directed RNA polymerase (EC 2.7.7.6) delta chain rpoE - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 31-Mar-1992 #sequence_revision 06-Feb-1995 #text_change 16-Jun-2000

C:Accession: JT0302; H32354; S55422; H69698

R: Lampe, M.; Binnie, C.; Schmidt, R.; Losick, R.

Gene 67, 13-19, 1988

A:Title: Cloned gene encoding the delta subunit of Bacillus subtilis RNA polymerase.

A:Reference number: JT0302; MUID:88329737; PMID:2843435

A:Accession: JT0302

A:Molecule type: DNA

A:Residues: 1-173 <L&M>

A:Cross-References: GB:M21677; NID:9143455; PIDN:AAA22710.1; PID:9143456

A:Note: Part of this sequence, including the amino end of the mature protein, was confir

R: Trach, K.; Chapman, J.W.; Pigott, P.; Lecocq, D.; Hoch, J.A.

J. Bacteriol. 170, 4194-4208, 1988

A:Title: Complete sequence and transcriptional analysis of the spoof region of the Bacil

A:Reference number: A91883; MUID:88314920; PMID:2457578

A:Accession: H32354

A:Molecule type: DNA

A:Residues: 143-173 <TRA>

A:Cross-References: GB:M22039; NID:9460910; PIDN:AAA16800.1; PID:9143596

R: Glaser, P.; Danchin, A.

submitted to the EMBL Data Library, May 1995

A:Description: Cloning and sequencing of the Bacillus subtilis chromosomal region from 3

A:Reference number: S55414

A:Accession: S55422

A:Molecule type: DNA

A:Residues: 1-173 <GLA>

A:Cross-References: EMBL:249782; NID:9853752; PIDN:CAA89869.1; PID:9853761

R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

A.: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall

iech, J.; Hatwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.

Koeleer, P.; Koningsstein, G.; Kirogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, R.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetlell

Rieger, M.; Rivolta, C.; Rooha, R.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Schroeter, E.; Scoffone, F.; Sekiguchi, Y.; Sekowska, A.; Serr

deuchi, M.; Tanakoshi, A.; Tanaka, H.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69698

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-173 <KUN>

A:Cross-References: GB:299123; GB:AL009126; NID:92636240; PIDN:CAR15744.1; PID:92636253

A:Experimental source: strain 168

C:Comment: This protein binds to the RNA polymerase core enzyme with or without a sigma

riulation.

C:Genetics:

A:Gene: rpoE

A:Start codon: TTG

C:Superfamily: DNA-directed RNA polymerase delta chain

C:Keywords: nucleotidyltransferase

F:2-173/Product: DNA-directed RNA polymerase delta chain #status experimental <MAT>

Alignment Scores:

Pred. No.:	155	Length:	173
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	1	Gaps:	0

US-09-817-318-1 (1-780) x JT0302 (1-173)

OY 760 GTAAGGCAAAAAAAAAA 780

Db 95 VallysAlalysLysLysLys 101

RESULT 27

A39022 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragments)

C:Species: Naja naja oxiana (Asian cobra, Oxis cobra)

C>Date: 06-Dec-1991 #sequence_revision 06-Dec-1991 #text_change 14-Nov-1997

C:Accession: A39022

R: Weise, C.; Kretzenkamp, H.J.; Raba, R.; Aaviksaar, A.; Hucho, F.

J. Protein Chem. 9, 53-57, 1990

A:Title: The active site and partial sequence of cobra venom acetylcholinesterase.

A:Reference number: A39022; MUID:90253585; PMID:2340076

A:Accession: A39022

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-173 <MER>

C:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: carboxylic ester hydrolase; glycoprotein

Alignment Scores:

Pred. No.:	155	Length:	173
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x A39022 (1-173)

OY 327 TTTTGCAGTGACTCTTTC 347

Db 59 PheLeuThrValThrLeuPhe 65

RESULT 28

S45548

hypothetical protein ypuF - Bacillus subtilis

C:Species: Bacillus subtilis

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 28-Jul-2000

C:Accession: S45548; E69942

R: Sorokin, A.; Zumbstein, E.; Azevedo, V.; Ehrlich, S.D.; Serror, P.

submitted to the EMBL Data Library, November 1993

A:Reference number: S45533

A:Accession: S45548

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <SOR>

A:Cross-References: EMBL:L09228; NID:9410114; PIDN:AAA67486.1; PID:9410130

R: Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber

C.: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal

iech, J.; Hatwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardiniois, A.; Althorst, Lamber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetille, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, akuchl, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchilyama, T.; Winters, P.; Wipit, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:96044033; PMID:9384377
A:Accession: E69942
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-174 <KUN>
A:Cross-references: GB:299116; GB:AL009126; NID:g2634723; PIDN:CAB14255.1; PID:ell85592;
A:Experimental source: strain 168
C:Genetics:
A:Gene: ypuF
A:Start codon: TTG
C:Superfamily: *Bacillus subtilis* hypothetical protein ypuF

Alignment Scores:
Pred. No.: 155 Length: 174
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x S45548 (1-174)

OY 603 TTATCTAATCTTTTGATT 583
|||||
Db 141 LeuSerAsnIlePheLeuVal 147

RESULT 29
D75514
hypothetical protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: D75514
R:White, O.; Eissen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75514
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-175 <WHI>
A:Cross-references: GB:AE001907; GB:AE000513; NID:g6456162; PIDN:AAFL0064.1; PID:g645817
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0481
A:Map position: 1

Alignment Scores:
Pred. No.: 155 Length: 175
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x D75514 (1-175)

OY 701 GTTTAATTCCTCGTTGTA 721
|||||
Db 4 ValLeuIleLeuValVal 10

RESULT 30
S14981

extensin class I (clone w1-8 L) - tomato (fragment)
C:Species: *Lycopersicon esculentum* (tomato)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 11-Jan-2000
C:Accession: S14981
R:Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A:Title: Tomato extensin and extensin-like cDNAs: structure and expression in respon
A:Reference number: S14970; MUID:91329690; PMID:1714316
A:Accession: S14981
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-199 <SHO>
A:Cross-references: EMBL:X55692
A:Experimental source: cv. UC82B
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: cell wall; glycoprotein; hydroxyproline

Alignment Scores:
Pred. No.: 153 Length: 199
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x S14981 (1-199)

OY 211 TTACCAATTCCTCCAAAAA 191
|||||
Db 23 LeuThrIleSerSerLysLys 29

RESULT 31
T31585
hypothetical protein Y48C3A.c - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C:Accession: T31585
R:Wallis, J.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21046
A:Accession: T31585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-206 <WLI>
A:Cross-references: EMBL:AL117203; PIDN:CAB55100.1; CESP:Y48C3A.c
A:Experimental source: clone Y48C3A
C:Genetics:
A:Gene: CESP:Y48C3A.c
A:Introns: 47/3; 89/2; 158/2
C:Superfamily: *Caenorhabditis elegans* hypothetical protein Y48C3A.c

Alignment Scores:
Pred. No.: 152 Length: 206
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T31585 (1-206)

OY 701 GTTTAATTCCTCGTTGTA 721
|||||
Db 30 ValLeuIleLeuValVal 36

RESULT 32
T17228
hypothetical protein DKFZP434D146.1 - human (fragment)
C:Species: *Homo sapiens* (man)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17228
R:Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999

A:Reference number: 218722
 A:Accession: T17228
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-211 <KOE>
 A:Cross-references: EMBL:AL117429
 A:Experimental source: adult testis; clone DKFZp434D146
 C:Genetics:
 A:Note: DKFZp434D146.1

Alignment Scores:
 Pred. No.: 152 Length: 211
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T17228 (1-211)

OY 526 CATTATGACCTGCTACTT 546
 DB 84 LeuphetThrLeuThrValLeu 90

RESULT 33

45997
 T45997
 Hypothetical protein F9D24.280 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 02-Sep-2000
 C:Accession: T45997
 R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, January 2000
 A:Reference number: 223011
 A:Accession: T45997
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <DAN>
 A:Cross-references: EMBL:AL137081
 A:Experimental source: cultivar Columbia; BAC clone F9D24
 C:Genetics:
 A:Map position: 3
 A:Introns: 85/3
 A:Note: F9D24.280
 C:Superfamily: Arabidopsis thaliana hypothetical protein F9D24.210

Alignment Scores:
 Pred. No.: 151 Length: 219
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x T45997 (1-219)

OY 760 GTAAGGCAAAAAAAAAAAAA 780
 DB 164 VallysAlaLysLysLysLys 170

RESULT 34

S59134
 S59134
 Probable zinc finger transcription activator Rep2 - fission yeast (Schizosaccharomyces fissionis)
 C:Species: Schizosaccharomyces pombe
 C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 31-Jan-2000
 C:Accession: S59134; T40130
 R:Nakashima, N.; Tanaka, K.; Sturm, S.; Okayama, H.
 EMO J. 14, 4794-4802, 1995
 A:Title: Fission yeast Rep2 is a putative transcriptional activator subunit for the cell cycle
 A:Reference number: S59134; PMID:96030785; PMID:7588609
 A:Accession: S59134
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-219 <NAK>

A:Cross-references: EMBL:X91044; NID:9975711; PIDN:CAA62504.1; PID:9975712
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A:Reference number: 221907
 A:Accession: T40130
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-219 <WOO>
 A:Cross-references: EMBL:Z97211; PIDN:CA10158.1; GSPDB:GN00067; SPDB:SPBC2F12.11c
 A:Experimental source: strain 972h-; cosmid c2F12
 C:Genetics:
 A:Gene: SPBC2F12.11c
 A:Map position: 2

Alignment Scores:
 Pred. No.: 151 Length: 219
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x S59134 (1-219)

OY 418 TCTCTGAGTCTCCTTCC 438
 DB 42 SerServalSerPheAla 48

RESULT 35

S40931
 S40931
 Hypothetical protein ZK1098.9 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
 C:Accession: S40931
 R:Thomas, K.
 submitted to the EMBL Data Library, February 1992
 A:Reference number: S40923
 A:Accession: S40931
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <THO>
 A:Cross-references: EMBL:Z22176; NID:9297978; PID:9297987
 C:Genetics:
 A:Introns: 48/1; 86/3; 111/3; 145/3; 188/3

Alignment Scores:
 Pred. No.: 151 Length: 220
 Score: 7.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.86% Indels: 0
 DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x S40931 (1-220)

OY 546 TGCAATGTATGCTAGATGT 566
 DB 183 CysIleValLeuLeuAspVal 189

RESULT 36

A10781
 A10781
 GTP cyclonucleotidylase I (EC 3.5.4.16) [imported] - Salmonella enterica subsp. enterica s.
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A10781
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 et al.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 et al.; Mouton, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608

A:Accession: A10781
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02575.1; PID:g16503433; GSPDB:GN00176
A:Gene: STY2427
C:Superfamily: GTP cyclohydrolase I
C:Keywords: hydrolase

Alignment Scores:
Pred. NO.: 151 Length: 222
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.86% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x A10781 (1-222)

OY 233 ACAGCTTACAGACCTTACTC 253
|||||
Db 161 ThrAlaLeuGlnThrLeu 167

RESULT 37
D89836
hypothetical protein SA0614 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89836
R:Kurodo, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Ii, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratazu, K.;
Lance 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89836
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-224 <KUR>
A:Cross-references: GB:BA000018; PID:g13700550; PIDN:BA041847.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0614
C:Superfamily: ompR protein; response regulator homology

Alignment Scores:
Pred. NO.: 151 Length: 224
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x D89836 (1-224)

OY 542 ACAGCATGTAATAGATTG 522
|||||
Db 193 ThrValAsnValAsnArgLeu 199

RESULT 38
G70000
two-component response regulator [ytsr] homolog ytsA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: G70000
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.: Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.: Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koelter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; S
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiy
T.: Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshid
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: G70000
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-231 <STO>
A:Cross-references: GB:D99119; GB:AL009126; NID:g2635411; PIDN:CAB15018.1; PID:g2635
A:Experimental source: strain 168
C:Genetics:
A:Gene: ytsA
C:Superfamily: ompR protein; response regulator homology
C:Keywords: phosphoprotein
F:4-112/Domain: response regulator homology <RRR>
F:52/Binding site: phosphate (asp) (covalent) #status predicted

Alignment Scores:
Pred. NO.: 151 Length: 231
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x G70000 (1-231)

OY 542 ACAGTCATGTAATAGATTG 522
|||||
Db 194 ThrValAsnValAsnArgLeu 200

RESULT 39
G84138
two-component response regulator BH3911 [imported] - Bacillus halodurans (strain C-1.
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: G84138
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; I
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: G84138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <STO>
A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA07630.1; GSPDB:
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3911
C:Superfamily: ompR protein; response regulator homology

Alignment Scores:
Pred. NO.: 151 Length: 231
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: 2 Gaps: 0

US-09-817-318-1 (1-780) x G84138 (1-231)

OY 542 ACAGTCATGTAATAGATTG 522
|||||
Db 194 ThrValAsnValAsnArgLeu 200

RESULT 40
S43513
hemoglobin linker chain 2 - polychaete (neanthes diversicolor) (fragment)

C:Species: Neanthes diversicolor
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 18-Aug-2000
C:Accession: S43513
R:Suzuki, T.; Ohla, T.; Yuasa, H.-J.; Takagi, T.
Biochim. Biophys. Acta 1217, 291-296, 1994
A:Title: The giant extracellular hemoglobin from the polychaete *Neanthes diversicolor*.
A:Reference number: S43513; MIMD:94198291; PMID:8148374
A:Accession: S43513
A:Molecule type: mRNA
A:Residues: 1-235 <SUZ>
A:Cross-references: EMBL:D58413; NID:g893395; PIDN:BAA09580.1; PID:d1010223; PID:g893395
C:Function: essential for assembly of heme containing subunits of extracellular giant
A:Note: annelid-like extracellular hemoglobins differ from all other vertebrate or non-
C:Superfamily: hemoglobin linker chain; LDL receptor ligand-binding repeat homology
F:68-106/Domain: LDL receptor ligand-binding repeat homology <LDL2>

Alignment Scores:
Pred. No.: 150 Length: 235
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x S43513 (1-235)
OY 470 TTGGGTATTTCAGAGACTG 450
|||||
Db 50 LeucylaspharagiuLeu 56

RESULT 41
D70032
two-component response regulator [YycQ] homolog yycP - *Bacillus subtilis*
C:Species: *Bacillus subtilis*
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: D70032
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berlet
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A: Ehlich, S.D.; Emmerson, P.T.; Eutian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
leeh, J.; Harwood, C.R.; Henalt, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koester, P.; Konungstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sdaile, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schreter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Ser
akuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MIMD:98044033; PMID:9384377
A:Accession: D70032
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-237 <KUN>
A:Cross-references: GB:299121; GB:AL009126; NID:g2635827; PIDN:CAB15477.1; PID:g2635985
A:Experimental source: strain 168
C:Genetics:
A:Gene: yycP
C:Superfamily: ompr protein; response regulator homology
C:Keywords: phosphoprotein
F:4-112/Domain: response regulator homology <RRH>
F:52/Binding site: phosphate (Asp) (covalent) #status predicted

Alignment Scores:
Pred. No.: 150 Length: 237
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x D70032 (1-237)
OY 542 ACAGTCATGTAATAGATG 522
|||||
Db 198 ThrValasValasArgLeu 204

RESULT 42
A81422
probable RNA polymerase sigma factor for flagellar operon Cj061c [imported] - *Campy*
C:Species: *Campylobacter jejuni*
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C:Accession: A81422
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chl
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanyliet, A.; Whitehead, S.; Bar
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals
A:Reference number: A81250; MIMD:20150912; PMID:10688204
A:Accession: A81422
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-238 <PAR>
A:Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72548.1; PID:g696
C:Genetics:
A:Experimental source: serotype O2, strain NCTC 11168
C:Superfamily: transcription initiation factor sigma; transcription initiation facto

Alignment Scores:
Pred. No.: 150 Length: 238
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.92% Indels: 0
DB: Gaps: 0

US-09-817-318-1 (1-780) x A81422 (1-238)
OY 330 AAATTCATGAGTCTGCAC 310
|||||
Db 182 LysIleHisGluValLeuasp 188

RESULT 43
A38379
phosducin, retinal - bovine
C:Species: *Bos primigenius taurus* (cattle)
C:Date: 28-Jun-1991 #sequence_revision 14-Jul-1994 #text_change 04-Oct-1996
C:Accession: A38379; J02025; A38378
R:Lee, R.H.; Fowler, A.; McGinnis, J.F.; Lolley, R.N.; Craft, C.M.
J. Biol. Chem. 265, 15867-15873, 1990
A:Title: Amino acid and cDNA sequence of bovine phosducin, a soluble phosphoprotein f
A:Reference number: A38379; MIMD:90368806; PMID:2203790
A:Accession: A38379
A:Molecule type: protein
A:Residues: 1-245 <LEE>
R:De, T.; Nakabayashi, H.; Tamada, H.; Takagi, T.; Sakuragi, S.; Yamaki, K.; Shinoha
Gene 91, 209-215, 1990
A:Title: Analysis of the human, bovine and rat 33-kDa proteins and cDNA in retina and
A:Reference number: J02025; MIMD:91007277; PMID:2210381
A:Accession: J02025
A:Molecule type: mRNA
A:Residues: 1-43, 'P', 45-238, 'K', 240-245 <ABE>
A:Cross-references: GB:M33529
R:Lee, R.H.; Brown, B.M.; Lolley, R.N.
J. Biol. Chem. 265, 15860-15865, 1990
A:Title: Protein kinase A phosphorylates retinal phosducin on serine 73 in situ.
A:Reference number: A38378; MIMD:90368805; PMID:2394752
A:Accession: A38378
A:Molecule type: protein
A:Residues: 54-58, 'X', 60-61, 'X', 63-64, 'XX', 67-70, 'X', 72-88, 'X', 90, 'X', 92-93, 102-114, '
C:Superfamily: phosducin
C:Keywords: glycoprotein; phosphoprotein; photoreceptor; retina
F:8, 58, 238/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status pre

F:45/69/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F:73/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status experimental
F:152/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Pred. No.:	150	Length:	245
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	1	Gaps:	0

US-09-817-318-1 (1-780) x A38379 (1-245)

QY 679 TTACTGACATTCATATCA 699

DB 197 LeuLeuSerAsnPhelIleSer 203

RESULT 44

G81297

hypothetical protein Cj1507c [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002

C:Accession: G81297

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Oual, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: G81297

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-245 <PAR>

A:Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73928.1; PID:g696893

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj1507c

C:Superfamily: Campylobacter jejuni hypothetical protein Cj1507c

Alignment Scores:

Pred. No.:	150	Length:	245
Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x G81297 (1-245)

QY 297 TTACAAAGATCTCAAGAA 317

DB 187 LeuGlnLysAsnSergInGln 193

RESULT 45

T17397

vr10 protein - Dichelobacter nodosus

C:Species: Dichelobacter nodosus

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000

C:Accession: T17397

R:Billington, S.J.; Huggins, A.S.; Johansen, P.A.; Crellin, P.K.; Cheung, J.K.; Katz, M
Infect. Immun. 67, 1277-1286, 1999

A:Title: Complete nucleotide sequence of the 27-kilobase virulence related locus (vrl) C

A:Reference number: Z18734; MUID:99150261; PMID:10024571

A:Accession: T17397

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-251 <BIL>

A:Cross-references: EMBL:U02046; NID:g3493323; PID:g2317810; PIDN:AAC33386.1

A:Experimental source: strain A198

C:Superfamily: Dichelobacter nodosus vrl0 protein

Alignment Scores:

Pred. No.:	149	Length:	251
------------	-----	---------	-----

Score:	7.00	Matches:	7
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.86%	Indels:	0
DB:	2	Gaps:	0

US-09-817-318-1 (1-780) x T17397 (1-251)

QY 312 CAGAGACTTCATGAATTTTG 332

DB 37 GlnGlnLeuHisGlnPhelLeu 43

Search completed: February 4, 2003, 07:23:29
Job time : 53 secs

